

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
1 April 2004 (01.04.2004)

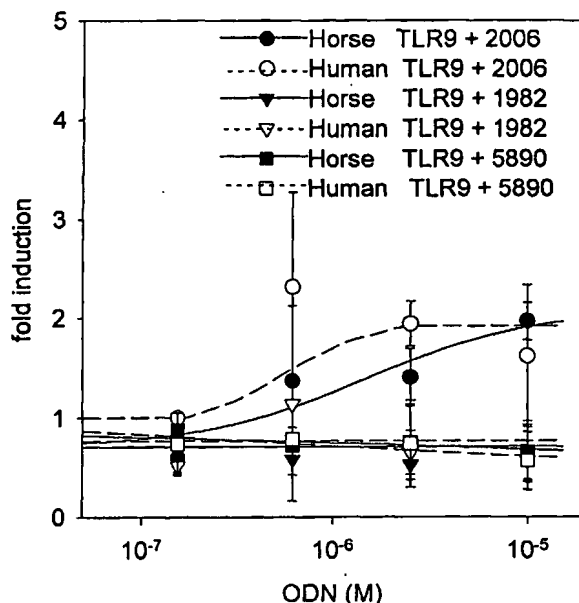
PCT

(10) International Publication Number
WO 2004/026888 A2

- (51) International Patent Classification⁷: **C07H** (72) Inventors; and
(75) Inventors/Applicants (for US only): **LIPFORD, Grayson, B.** [US/US]; 38 Bates Road, Watertown, MA 02472 (US). **MOOKHERJEE, Neeloffer** [IN/CA]; Apt 408, 2233 Allison Road,, Vancouver, BC V6T 1T7 (CA). **BABIUK, Lorne** [CA/CA]; 245 East Place, Saskatoon, Saskatchewan S7J 2Y1 (CA). **BROWNLIE, Robert** [CA/CA]; 123 O'Brien Crescent, Saskatoon, Saskatchewan S7K 5K3 (CA). **GRIEBEL, Philip** [CA/CA]; Box 36, RR5, Saskatoon, Saskatchewan S7K 3J8 (CA). **MUTWIRI, George** [CA/CA]; 569 Nordstrum Road, Saskatoon, Saskatchewan S7K 7X6 (CA). **HECKER, Rolf** [DE/DE]; Benröderstr. 60, 40597 Düsseldorf (DE).
- (21) International Application Number: **PCT/US2003/029577**
- (22) International Filing Date:
19 September 2003 (19.09.2003)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
60/412,479 19 September 2002 (19.09.2002) US
- (71) Applicants (for all designated States except US): **COLEY PHARMACEUTICAL GMBH** [DE/DE]; Elisabeth-Selbert-Strasse 9, 40764 Langenfeld (DE). **UNIVERSITY OF SASKATCHEWAN** [CA/CA]; Kirk Hall, 117 Science Place, Saskatoon, Saskatchewan S7N 5C8 (CA). **QIAGEN GMBH** [DE/DE]; Max-Volmer-Strasse 4, 40724 Hilden (DE).
- (74) Agent: **STEELE, Alan, W.**; Wolf, Greenfield & Sacks, P.C., 600 Atlantic Avenue, Boston, MA 02210 (US).
- (81) Designated States (national): AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX,

[Continued on next page]

(54) Title: TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES



(57) Abstract: Novel amino acid and nucleotide sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) Toll-like receptor 9 (TLR9) are provided. Also provided are amino acid and nucleotide sequences for dog (canine), cat (feline), mouse (murine), and human TLR9. Comparison of these sequences, especially in combination with functional assessment for species-specific CpG motif preferences, permits identification of specific regions and amino acid residues of interest in TLR9 ligand interaction. Novel chimeric TLR9 receptor molecules, cells expressing these molecules, and methods for their use in screening assays for TLR9 ligands are also provided.



MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO,

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

Background of the Invention

Synthetic oligodeoxynucleotides (ODN) and DNA containing immunostimulatory
5 CpG motifs (CpG DNA) function as potent adjuvants and activators of the innate immune
system. Heeg K et al. (2000) *Int Arch Allergy Immunol* 121:87-97; Krieg AM (2001)
Vaccine 19:618-22. A wide variety of CpG-containing sequences have been screened for
biological activity and it is reported that optimal CpG DNA sequences can vary among
species. Rankin R et al. (2001) *Antisense Nucleic Acid Drug Dev* 11:333-40.

10 Toll-like receptor 9 (TLR9) has recently been identified as a receptor for CpG ODN.
Hemmi H et al. (2000) *Nature* 408:740-5. The molecular mechanism by which TLR9
recognizes CpG DNA is not understood.

Summary of the Invention

15 Toll-like receptor 9 (TLR9) is known to be involved in innate immunity and to signal
in response to CpG DNA. To date, the amino acid sequences only of human and murine
TLR9 have been reported, and, interestingly, these two species are known to prefer different
CpG motifs. The structural basis for this species-specific CpG motif preference has not yet
been fully elucidated. The instant invention provides, in part, novel amino acid and
20 nucleotide sequences of rat, pig, cow, and horse TLR9. These novel TLR9 sequences are
useful for elucidating certain key structural features of TLR9. Specifically, comparison of
sequences of murine, human, and these novel TLR9 sequences permits identification of areas
of highly conserved sequence, areas of group conservation, and areas of hypervariability. In
addition, such comparisons permit an assessment of evolutionary relatedness among TLR9
25 molecules of the various species, as well as an assessment of inter-species homologies.
Importantly, such comparisons permit a rational basis for identifying amino acids in TLR9
that may be involved in the CpG binding site, as well as amino acids involved in conferring
species specificity for particular CpG motifs. Such information may be used to design and
construct novel TLR9 molecules which incorporate specific point or regional mutations and
30 which possess desired ligand binding characteristics. Such information may also be useful in
designing and identifying novel ligands for TLR9 of a given species.

- 2 -

In one aspect, the invention provides isolated polypeptides having amino acid sequences for rat, pig (porcine), cow (bovine), horse (equine), and sheep (ovine) TLR9 polypeptides. These amino acid sequences correspond to SEQ ID NOs 1, 5, 9, 13, and 17, respectively. Each of these sequences is believed to include at least a majority of an
5 extracellular domain, as well as a transmembrane region and at least part of a TLR/IL-1 receptor (TIR) domain. To the extent any such sequence may lack an amino-terminal and/or carboxy-terminal sequence, such sequence is ascertainable, without undue experimentation, using conventional molecular biology techniques and the sequence information provided herein.

10 In another aspect the invention provides isolated polypeptides having amino acid sequences for essentially the whole extracellular domain, optionally including a signal peptide, of each of rat, porcine, bovine, equine, and ovine TLR9. These amino acid sequences correspond to SEQ ID NOs 2, 6, 10, 14, and 18, respectively. Such extracellular domains are believed to include sequence specifically involved in binding to TLR9 ligand,
15 such as CpG DNA. In addition, such extracellular domains are believed to include sequence that confers species specificity for particular CpG motifs.

Isolated nucleic acid molecules encoding the polypeptides just described above are also provided according to further aspects of the invention. Such nucleic acid molecules include, but are not limited to, nucleic acid molecules having sequences provided by SEQ ID
20 NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively. Isolated nucleic acid molecules encoding the TLR9 polypeptides of SEQ ID NOs 1, 5, 9, 13, 17; and 2, 6, 10, 14, and 18 also include nucleic acid molecules that differ in sequence from SEQ ID NOs 3, 7, 11, 15, 19; and 4, 8, 12, 16, and 20, respectively, due to degeneracy of the genetic code. Such nucleic acid molecules will hybridize, under stringent conditions, with suitably selected nucleic acid
25 molecules having sequences selected from SEQ ID NOs 3, 4, 7, 8, 11, 12, 15, 16, 19, and 20.

In another aspect the invention provides a vector which includes an isolated nucleic acid molecule of the invention. In one embodiment the vector is an expression vector and the isolated nucleic acid molecule of the invention is operably linked to a regulatory sequence in the vector. When present within a cell, an expression vector according to this aspect of the
30 invention causes the cell to express a polypeptide of the invention.

The invention according to another aspect provides a cell in which a vector of the invention is present. In one embodiment the cell containing the vector expresses a

- 3 -

polypeptide of the invention. In certain embodiments the cell also contains a reporter construct that transduces a TLR9-mediated signal in response to contact of the polypeptide of the invention or a TLR9 with a suitable TLR9 ligand. The cell containing the vector, and optionally containing the reporter construct, can be used in screening methods also provided
5 by the invention.

In yet another aspect the invention provides an antibody or antibody fragment that binds specifically to an isolated polypeptide of the invention. In certain embodiments the antibody or antibody fragment binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide. More specifically, the antibody or antibody fragment binds uniquely to
10 one of the isolated polypeptides of the invention. In one embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide also binds to either mouse or human TLR9. In another embodiment the antibody or antibody fragment that binds uniquely to one of rat, porcine, bovine, equine, or ovine TLR9 polypeptide does not also bind to either mouse or human TLR9. In some embodiments
15 the antibody or antibody fragment binds selectively to a chimeric TLR9 polypeptide of the invention. In certain embodiments the antibody or antibody fragment of the invention is a monoclonal antibody or fragment of a monoclonal antibody.

In one aspect the invention provides a method for identifying key amino acids in a TLR9 of a first species which confer specificity for CpG DNA optimized for TLR9 of the
20 first species. The method involves aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species; generating an initial set of candidate amino acids in the TLR9 of the
25 first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with the TLR9 of the third species or (b)
30 differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

- 4 -

In another aspect the invention provides a method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9. The method according to this aspect of the invention involves aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a CpG DNA optimized for murine TLR9; generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution; generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids. In one embodiment the method according to this aspect of the invention is performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred CpG DNA).

In another aspect the invention also provides an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (extracellular domain (ECD) of murine TLR9) except for substitution of at least one key amino acid identified according to the method above. The polypeptide according to this aspect of the invention is a chimeric TLR9 polypeptide. Preferably the polypeptide according to this aspect of the invention binds to CpG DNA optimized for human TLR9 better than does the isolated polypeptide having an amino acid sequence identical to SEQ ID NO:30 (ECD of murine TLR9). In one embodiment the polypeptide includes only one substituted amino acid. The isolated polypeptide according to this aspect of the invention may further include sequence involved in TLR/IL-1R signal transduction, e.g., intracellular domain of TLR9 as provided in SEQ ID NOs 29 and 33. For example, in one embodiment a polypeptide according to this aspect of the invention is an isolated polypeptide having an amino acid sequence identical to SEQ ID NO:29 (full length murine TLR9) except for substitution of at least one key amino acid identified according to the method above.

- 5 -

In another aspect the invention provides an isolated nucleic acid molecule including a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described. In one embodiment the isolated nucleic acid molecule has a nucleic acid sequence encoding a chimeric TLR9 polypeptide just described.

5 In yet another aspect, the invention provides a screening method to identify a TLR9 ligand. The method involves contacting a polypeptide (including a chimeric TLR9 polypeptide) of the invention with a candidate TLR9 ligand; measuring a signal in response to the contacting; and identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling. In one embodiment
10 the candidate TLR9 ligand is an immunostimulatory nucleic acid. In one embodiment the candidate TLR9 ligand is a CpG DNA.

The invention also provides, in yet a further aspect, a screening method to identify species-specific CpG-motif preference of an isolated polypeptide of the invention. The method according to this aspect of the invention involves contacting an isolated polypeptide
15 of the invention with a CpG DNA including a hexamer sequence selected from the group consisting of GACGTT, AACGTT, CACGTT, TACGTT, GGCGTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG; measuring a signal in response to the contacting; and identifying a species-specific CpG-motif preference when the signal in
20 response to the contacting is consistent with TLR9 signaling. In one embodiment the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

	TCCATGACGTTTTTGATGTT	(SEQ ID NO:39),
	TCCATAACGTTTTTGATGTT	(SEQ ID NO:40),
	TCCATCACGTTTTTGATGTT	(SEQ ID NO:41),
25	TCCATTACGTTTTTGATGTT	(SEQ ID NO:42),
	TCCATGGCGTTTTTGATGTT	(SEQ ID NO:43),
	TCCATGCCGTTTTTGATGTT	(SEQ ID NO:44),
	TCCATGTCGTTTTTGATGTT	(SEQ ID NO:45),
	TCCATGATGTTTTTGATGTT	(SEQ ID NO:46),
30	TCCATGAAGTTTTTGATGTT	(SEQ ID NO:47),
	TCCATGAGGTTTTTGATGTT	(SEQ ID NO:48),
	TCCATGACATTTTTGATGTT	(SEQ ID NO:49),
	TCCATGACCTTTTTGATGTT	(SEQ ID NO:50),
	TCCATGACTTTTTTGATGTT	(SEQ ID NO:51),
35	TCCATGACGCTTTTGATGTT	(SEQ ID NO:52),
	TCCATGACGATTTTGATGTT	(SEQ ID NO:53),
	TCCATGACGGTTTTGATGTT	(SEQ ID NO:54),

- 6 -

TCCATGACGTCTTTGATGTT (SEQ ID NO:55),
 TCCATGACGTATTTGATGTT (SEQ ID NO:56), and
 TCCATGACGTGTTTGATGTT (SEQ ID NO:57).

In certain embodiments of the screening methods of the invention, the signal includes
 5 expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway. In one
 embodiment the reporter gene is operatively linked to a promoter sensitive to NF- κ B. In one
 embodiment the signal in response to contacting is binding of the candidate TLR9 ligand or
 CpG DNA to the polypeptide of the invention.

In one embodiment the screening method is performed on a plurality of test
 10 compounds. In one embodiment the response mediated by the TLR9 signal transduction
 pathway is measured quantitatively and the response mediated by the TLR9 signal
 transduction pathway associated with each of the plurality of test compounds is compared
 with a response arising as a result of an interaction between the functional TLR9 and a
 reference immunostimulatory compound.

15 Brief Description of the Figures

Figure 1 depicts a Clustal W multiple sequence alignment of deduced amino acid
 sequences for cat (feline), dog (canine), cow (bovine), mouse (murine), sheep (ovine), pig
 (porcine), horse (equine), human, and rat TLR9 polypeptides. The deduced amino acid
 20 sequences for feline, canine, bovine, murine, ovine, porcine, equine, human, and rat TLR9
 polypeptides shown in the figure correspond to SEQ ID NOs 25, 21, 9, 29, 17, 5, 13, 33, and
 1, respectively. Lines labeled "multiple" refer to the multiple sequence alignment of all six
 sequences shown. Lines labeled "mo/hu" refer to a paired sequence alignment of mouse and
 human TLR9 sequences alone.

25 Figure 2 is a cladogram depicting an evolutionary relatedness tree for rat, murine,
 porcine, bovine, equine, and human TLR9 polypeptides in Figure 1.

Figure 3 is a graph depicting species specificity of TLR9 signaling with selected
 oligonucleotides having strong specificity for human (2006), mouse (5890), or neither (1982).

30 Detailed Description of the Invention

The present invention provides novel amino acid and nucleotide sequences for TLR9
 derived from rat, pig, cow, horse, and sheep. These sequences can be used to identify key
 features of the primary sequences of these and related TLR molecules, including previously

- 7 -

known primary sequences of human and mouse (murine) TLR9. Such key features include binding site information and species specificity toward particular CpG motifs. Native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to identify and to design novel TLR9 ligands.

5 Additionally, the native and novel chimeric TLR9 polypeptides designed with the aid of this information can be expressed in vitro or in vivo and used in screening assays to compare various TLR9 ligands, including CpG DNA.

In one aspect the invention provides isolated TLR9 polypeptides, and isolated nucleic acid molecules encoding them, from rat, pig, cow, horse, and sheep. The term "isolated" as
10 used herein with reference to a nucleic acid molecule or polypeptide means substantially free of or separated from components with which it is normally associated in nature, e.g., other nucleic acids, proteins, lipids, carbohydrates or *in vivo* systems to an extent practical and appropriate for its intended use. In particular, the nucleic acids or polypeptides are sufficiently pure and are sufficiently free from other biological constituents of host cells so as
15 to be useful in, for example, producing pharmaceutical preparations. Because an isolated nucleic acid or polypeptide of the invention may be admixed with a pharmaceutically acceptable carrier in a pharmaceutical preparation, the nucleic acid or polypeptide may represent only a small percentage by weight of such a preparation. The nucleic acid or polypeptide is nonetheless substantially pure in that it has been substantially separated from
20 the substances with which it may be associated in living systems.

An amino acid sequence of rat TLR9 is provided as SEQ ID NO:1. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:1 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of rat TLR9 (See
25 Figure 1). Amino acids numbered 1-821 of SEQ ID NO:1 are presumptively extracellular domain and correspond to SEQ ID NO:2. SEQ ID NO:3 is a nucleotide sequence of rat TLR9 cDNA having an open reading frame corresponding to nucleotides 1-3096. SEQ ID NO:4 is a nucleotide sequence of rat cDNA encoding amino acids 1-821 of SEQ ID NO:1.

An amino acid sequence of porcine TLR9 is provided as SEQ ID NO:5. Based on
30 comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:5 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of porcine TLR9

- 8 -

(See Figure 1). Amino acids numbered 1-819 of SEQ ID NO:5 are presumptively extracellular domain and correspond to SEQ ID NO:6. SEQ ID NO:7 is a nucleotide sequence of porcine TLR9 cDNA having an open reading frame corresponding to nucleotides 77-3166. SEQ ID NO:8 is a nucleotide sequence of porcine cDNA encoding amino acids 1-819 of SEQ ID NO:5.

An amino acid sequence of bovine TLR9 is provided as SEQ ID NO:9. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:9 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of bovine TLR9

(See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:9 are presumptively extracellular domain and correspond to SEQ ID NO:10. SEQ ID NO:11 is a nucleotide sequence of bovine TLR9 cDNA having an open reading frame corresponding to nucleotides 84-3170. SEQ ID NO:12 is a nucleotide sequence of bovine cDNA encoding amino acids 1-818 of SEQ ID NO:9.

An amino acid sequence of equine TLR9 is provided as SEQ ID NO:13. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:13 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of equine TLR9

(See Figure 1). Amino acids numbered 1-820 of SEQ ID NO:13 are presumptively extracellular domain and correspond to SEQ ID NO:14. SEQ ID NO:15 is a nucleotide sequence of equine TLR9 cDNA having an open reading frame corresponding to nucleotides 115-3207. SEQ ID NO:16 is a nucleotide sequence of equine cDNA encoding amino acids 1-820 of SEQ ID NO:13.

An amino acid sequence of ovine TLR9 is provided as SEQ ID NO:17. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:17 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of ovine TLR9 (See Figure 1). Amino acids numbered 1-818 of SEQ ID NO:17 are presumptively extracellular domain and correspond to SEQ ID NO:18. SEQ ID NO:19 is a nucleotide sequence of ovine TLR9 cDNA having an open reading frame corresponding to nucleotides 92-3178. SEQ ID NO:20 is a nucleotide sequence of ovine cDNA encoding amino acids 1-818 of SEQ ID NO:17.

- 9 -

SEQ ID NO:1 (Rat TLR9)

5 MVLCRRTLHPLSLLVQAAVLAEALALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAAEPRSNITSLSLIANRI
HHLHNLDFVHLPNVRQLNLKWNCPPLGLSPLHFSCRMTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL
SHTNIVLVDASSLAGLHSLRVLFMDGNCYYKNPCNGAVNVTPDAFLGLSNLTHLSLKYNNTLTVPRQLPPSLEYL
10 LLSYNLIVKLGAEDLANLTSLRMLDVGGNCRRCDHAPDLCTECRQKSLDLHPQTFHHLSHLEGLVLKDSSLHSLN
SKWFQGLANLSVLDLSENFLYESINKTSFAQNLTRLRKLDLSFNKYCKVSFARLHLASSFKSLVSLQELNMNGIF
FRLLNKNTLRWLAGLPKLHTLHLQMNFINQAQLSVFSTFRALRFVDLSNNRISGPPTLSRVAPEKADEAEKGVWP
PASLTPALPSTPVSKNFMVRCKNLRFMTDLNRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK
15 VLDLSYNKLDLYHSKSFSELPQLQALDLSYNSQPFMSQIGHNFSFLANLSRLQNLSLAHNDIHSRVSSRLYSTS
VEYLDGSGNGVGRMWDEEDLYLYFFQDLRSLIHLDLSONKLHILRPQNLNLYLPKSLTKLSFRDNHLSFFNWSSLA
FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVPFAFFALAVELKEVNLSHNILKTVDRSWFGPIV
MNLTVLDVSSNPLHCACGAPFVDLLLEVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFGLSLL
AVAVGTVLPPLLQHLGWDVWYCFHLCCLAWLPLLTRGRRSAQALPYDAFVVDKAQSAVADWVYNELRVRLERERG
20 RRALRLCLEDRDWLPGQTLFENLWASIYGSRKTLFVLAHTDKVSGLLRTSFLLAQQRLLLEDKDVVVLVILRPDA
HRSRYVRLRQLCRQSVLFWPHQPNGQGSFWAQLSTALTRDNHFFYNRNFCRGPTAE

SEQ ID NO:2 (Rat TLR9)

20 MVLCRRTLHPLSLLVQAAVLAEALALGTLPAFLPCELKPHGLVDCNWLFLKSVPHFSAAEPRSNITSLSLIANRI
HHLHNLDFVHLPNVRQLNLKWNCPPLGLSPLHFSCRMTIEPKTFLAMRMLEELNLSYNGITTVPRLPSSLTNLSL
SHTNIVLVDASSLAGLHSLRVLFMDGNCYYKNPCNGAVNVTPDAFLGLSNLTHLSLKYNNTLTVPRQLPPSLEYL
LLSYNLIVKLGAEDLANLTSLRMLDVGGNCRRCDHAPDLCTECRQKSLDLHPQTFHHLSHLEGLVLKDSSLHSLN
SKWFQGLANLSVLDLSENFLYESINKTSFAQNLTRLRKLDLSFNKYCKVSFARLHLASSFKSLVSLQELNMNGIF
25 FRLLNKNTLRWLAGLPKLHTLHLQMNFINQAQLSVFSTFRALRFVDLSNNRISGPPTLSRVAPEKADEAEKGVWP
PASLTPALPSTPVSKNFMVRCKNLRFMTDLNRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFLPLTNLK
VLDLSYNKLDLYHSKSFSELPQLQALDLSYNSQPFMSQIGHNFSFLANLSRLQNLSLAHNDIHSRVSSRLYSTS
VEYLDGSGNGVGRMWDEEDLYLYFFQDLRSLIHLDLSONKLHILRPQNLNLYLPKSLTKLSFRDNHLSFFNWSSLA
FLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVPFAFFALAVELKEVNLSHNILKTVDRSWFGPIV
MNLTVLDVSSNPLHCACGAPFVDLLLEVQTKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLSRDCFG
30

SEQ ID NO:3 (Rat TLR9)

atggttctctgtctgcaggaccctgcaccccttgtctctcctggtagacaggccgcagtgctggctgaggctctggcc
ctgggtaccctgcctgccttctaccctgtgaactgaagcctcatggcctggtagactgcaactggctcttctctg
aagtctgtgcctcacttctctgcccagacaccccggtccaacatcaccagccttctccttgatcgccaaccgcac
35 caccacctgcacaacctcgacttctgcccacctgcccacagtgccgacagctgaacctcaagtggaaactgtccgccc
cctggcctcagccccttgcaacttctcctgcccgcacgacattgagcccaaaccttctcctggctatgcccacgctg
gaagagctgaacctgagctataacggtatcaccactgtgccccgcctgcccagctccctgacgaatctgagccta
agccacaccaacatcctggtagctgcccagcagcctcgctggcctgcacagcctgcagagttctcttcatggac
gggaactgctactacaagaacccctgcaacggggcggtgaacgtgaccccgagccttctcctgggcttgagcaac
40 ctacccacttgccttaagtataacaacctcacagaggtgccccgccaactgccccccagcctggagtagctc
ctgctgtcctataacctcatcgtaagctgggggcccgaagacctagccaacctgacctcccttcgaatgcttgat
gtgggtgggaattgcccgtcgctgtgatcacgccccgacctctgtacagaatgccggcagaagtcccttgatctg
caccctcagactttccatcacctgagccacctgaaggcctgggtgctgaaggacagttctctccactcgctgaac
tccaagtgggtccagggtctggcgaaacctctcggtgctggacctgaagcgagaacttctctacgagagcatcaac
45 aaaacagcgcccttccagaacctgaccctgctgcgaagctcgacctgtccttcaattactgcaagaaggatcg
ttcgcccgccctccacctggcaagttccttcaagagcctgggtgctcgctgcaggagctgaacatgaacggcatctt
ttcgcttactcaacaagaacacgctcaggtggctggctggctgctgcccaagctccacacgctgcaccttcaaatg
aatttcatcaaccaggcgagctcagcgtctttagtaccttccgagcccttcgcttctgtggacctgtccaataat
cgcatcagcgggctccaacgctgtccagagctgcccccgaaaaggcagacgaggcgaggaaggggttccatgg
50 cctgcaagtctcaccacgctctcccagacactcccgtctcaagaacttcatggctcaggtgtaagaacctcaga
ttcaccatggacctgtctcggaacaaccaggtgactatcaagccagagatgttcgtcaacctctcccatctccag
tgtctgagcctgagccacaactgcacgcgaggtgtcaatggctctcagttcctgcccgtgaccaacctgaag
gtgctggacctgtcctataacaagctggacctgtaccattcgaaatcgctcagtgagctccacagttgcaggcc

- 10 -

ctggacctgagctacaacagccagccattcagcatgcaggggataggccacaacttcagttttctggccaatctg
tccagggttacagaaccttagcctggcacacaatgacattcacagccgctgtcctcacgcctctacagcacctca
gtggagtatctggacttcagcggcaacggtgtgggcccgcagtggtgggacgaggaggacctttacctctatttcttc
5 caagacctgagaagcctgattcatctggacctgtctcagaataagctgcacatcctccggccccagaacctcaac
tacctccccaagagcctgacgaagctgagtttccgtgacaatcacctctctttctttaactggagcagtctggcc
ttcctgccaatctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcaccctgccta
ggcagctcctccagaaaactggatgtcagtagcaacagtatcgtctttgtgggtcccagccttctttgctctggcg
gtagagctaaaagaggtcaacctcagccataacatcctcaagactgtggatcgctcctgggtttgggcccattgtg
10 atgaacctgacggttctagacgtgagcagcaacctctgcattgtgcctgcggtgcaccctttgtagacttactg
ctggaagtgcagaccaaggtgcctggcctggctaacggtgtgaagtgtggcagtcctccgcccagctgcagggccgc
agcatctttgcgcaagacctgcggtgtgcctggatgacgtcctttctcgggactgctttggcctttcactcctg
gctgtggcgtgggcacggtgttgccctttactgcagcatctctgcggtgggacgtctggtactgtttccatctg
tgccctggcatggctacctttgctgacctggcggcgagcgcaccaagctctcccttatgatgccttcgtggtg
15 ttcgataaggcgagagcggttgctgactgggtgtataacgagcttcgagtgcggtgtaggagcggtgcggtg
cgccgagccctacgcttgtgtctggaggaccgagattggctgcctggccagacactcttcgagaacctctggg
tccatctatggcagccgcaagactctgtttgtgctggccacacggacaaggtcagtgccctcctgcgcaccagc
ttcctgctggctcagcagcgctgctggaggaccgcaaggacgtggtggtgtggtgatcctgcgcctgatgcc
caccgctcccgctacgtgcgactgcgccagcgctctgcgcagagtggtctcttctggcccatcagcccaac
20 gggcagggcagcttctgggcccagctgagtacagccctgactagggacaaccaccacttctataaccggaacttc
tgccggggacctacagcagaatag

SEQ ID NO:4 (Rat TLR9)

atggttctctgtcgcaggacctgcaccccttgtctctcctggtagaggccgcagtgctggctgaggctctggcc
ctgggtacctgtcctgccttccctacctgtgaactgaagcctcatggcctggtagactgcaactggctcttctcctg
25 aagtctgtgcctcacttctctgcccagaaacccgttccaacatcaccagccttctccttgatgcgcaaccgcatc
caccacctgcacaacctcgactttgtccacctgcccacgtgcgacagctgaacctcaagtggaaactgtccgccc
cctggcctcagcccttgacttctcctgcgcagtgaccattgagcccaaaccttctggctatgcgcatgctg
gaagagctgaacctgagctataacggtatcaccactgtgccccgcctgcccagctcctgacgaatctgagccta
agccacaccaacatcctggtactcgatgccagcagcctcgctggcctgcacagcctgcgagttctcttcatggac
30 gggaaactgctactacaagaacccctgcaacggggcggtgaacgtgaacccggacgccttctgggcttgagcaac
ctcaccacttgtcccttaagtataacaacctcacagaggtgccccgccaactgccccccagcctggagtacctc
ctgctgtcctataacctcatcgtcaagctgggggcccgaagacctagccaacctgacctccttctgaatgcttgat
gtgggtgggaattgcccgtcgctgtgatcacgccccgacctctgtacagaatgcgggcagaagtccttgatctg
caccctcagactttccatcacctgagccaccttgaaggcctgggtgctgaaggacagttctctccactcgctgaac
35 tccaagtgggtccagggtctggcgaacctctcggtgctggacctaaagcgagaacttctctacgagagcatcaac
aaaaccagcgcttctcagaacctgacctgtgcgcaagctcgacctgtccttcaattactgcaagaaggtatcg
ttcgcccgctccacctggcaagttccttcaagagcctgggtgtcgctgcaggagctgaacatgaacggcatcttc
ttccgcttactcaacaagaacacgctcaggtggctggctggctgtgcccagctccacacgctgcaccttcaaatg
aatttcatcaaccaggcgagctcagcgtcttttagtaccttccgagcccttcgctttgtggacctgtccaataat
40 cgcacagcgggctccaacgctgtccagagtcgccccgaaaaggcagacgagggcgagaaggggttccatgg
cctgcaagctcaccacagctctcccagcactcccgctctcaaagaacttcatggtcaggtgtaagaacctcaga
ttcaccatggacctgtctcggaacaaccaggtgactatcaagccagagatgttcgtcaacctctccatctccag
tgtctgagcctgagccacaactgcacgcaggtgtcaatggctctcagttcctgcccgtgaccaacctgaag
gtgctggacctgtcctataacaagctggacctgtaccattcgaaatcggttcagtgagctcccacagttgcaggcc
45 ctggacctgagctacaacagccagccattcagcatgcaggggataggccacaacttcagtttcttgccaatctg
tccagggttacagaaccttagcctggcacacaatgacattcacagccgctgtcctcacgcctctacagcacctca
gtggagtatctggacttcagcggcaacggtgtgggcccgcagtggtgggacgaggaggacctttacctctatttcttc
caagacctgagaagcctgattcatctggacctgtctcagaataagctgcacatcctccggccccagaacctcaac
tacctccccaagagcctgacgaagctgagtttccgtgacaatcacctctctttctttaactggagcagtctggcc
50 ttcctgccaatctgcgagacctggacctggcaggcaatctactaaaggccctgaccaacggcaccctgccta
ggcagctcctccagaaaactggatgtcagtagcaacagtatcgtctttgtgggtcccagccttctttgctctggcg
gtagagctaaaagaggtcaacctcagccataacatcctcaagactgtggatcgctcctgggtttgggcccattgtg
atgaacctgacggttctagacgtgagcagcaacctctgcattgtgcctgcggtgcaccctttgtagacttactg
ctggaagtgcagaccaaggtgcctggcctggctaacggtgtgaagtgtggcagtcctccgcccagctgcagggccgc
55 agcatctttgcgcaagacctgcggtgtgcctggatgacgtcctttctcgggactgctttggc

- 11 -

SEQ ID NO:5 (Porcine TLR9)

MGPRCTLHPLSLLVQVTALAAALAQGRLPAPFLPCELQPHGLVNCNWLFLKSVPHFSAAAPRANVTSLSLLSNRIH
 HLHDSDFVHLSSLRTLNLKWNCPAGLSPMHFPCCHMTIEPNTFLAVPTLEELNLSYNSITTVPALPDSLVSLSLS
 RTNILLVDPTHLTGLHALRYLYMDGNCYKNPCQGALEVVPGALLGLGNLTHLSLKYNMLTEVPRSLPPSLETLL
 5 LSYNHIVTLTPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKDHKLHSDTFSHLSRLEGLVLKDSSLYNLDT
 RWFRGLDRLQVLDLSENFYDCITKTAFQGLARLRLSLNLSFNHYHKKVSFAHLHLAPSFGLHRLSLKELDMHGIF
 RSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLYVDLSDNRISGAARPVAITREVDGRERVWLPSR
 NLAPRPLDTRLSED FMPNCKAFSFTLDLSRNNLVTIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVL
 10 DLSHNKL DLYHGRSFTLPRLEALDLSYNSQPFMTQGVGHNL SFVAQLPALRYLSLAHNDIHSRVSQQLCSASLC
 ALDFSGNDLSRMWAEGDLYLRFFQGLRSLVWLDLSQNHHLHTLLPRALDNLPKSLKHLHLRDNNAFFNWSSLTLL
 PKLETLDLAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNPGFFALAKQLEELNLSANALKTVEPSWFGSMVGN
 LKVLVDVSANPLHCACGATFVGFLLEVQAAVPGLPSRVKCGSPGQLQGHSIFAQDLRLCLDETLSWNCFGISLLAM
 ALGLVVPMLHHLHCGWDLWYCFHLCLAWLPHRGQRRGADALFYDAFVVDKAQSAVADWVYNELRVQLEERRGRRA
 15 LRLCLEERDWLPGKTLFENLWASVYSSRKTFLVLAHTDRVSGLLRASFLLAQQRLLLEDKDVVVLVILRPDAYRS
 RYVRLRQRLCRQSVLLWPHQPRGQGSFWAQLGTALTRDNHFFYNRNFRCRGPPTAE

SEQ ID NO:6 (Porcine TLR9)

MGPRCTLHPLSLLVQVTALAAALAQGRLPAPFLPCELQPHGLVNCNWLFLKSVPHFSAAAPRANVTSLSLLSNRIH
 HLHDSDFVHLSSLRTLNLKWNCPAGLSPMHFPCCHMTIEPNTFLAVPTLEELNLSYNSITTVPALPDSLVSLSLS
 20 RTNILLVDPTHLTGLHALRYLYMDGNCYKNPCQGALEVVPGALLGLGNLTHLSLKYNMLTEVPRSLPPSLETLL
 LSYNHIVTLTPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKDHKLHSDTFSHLSRLEGLVLKDSSLYNLDT
 RWFRGLDRLQVLDLSENFYDCITKTAFQGLARLRLSLNLSFNHYHKKVSFAHLHLAPSFGLHRLSLKELDMHGIF
 RSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLYVDLSDNRISGAARPVAITREVDGRERVWLPSR
 25 NLAPRPLDTRLSED FMPNCKAFSFTLDLSRNNLVTIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVL
 DLSHNKL DLYHGRSFTLPRLEALDLSYNSQPFMTQGVGHNL SFVAQLPALRYLSLAHNDIHSRVSQQLCSASLC
 ALDFSGNDLSRMWAEGDLYLRFFQGLRSLVWLDLSQNHHLHTLLPRALDNLPKSLKHLHLRDNNAFFNWSSLTLL
 PKLETLDLAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNPGFFALAKQLEELNLSANALKTVEPSWFGSMVGN
 LKVLVDVSANPLHCACGATFVGFLLEVQAAVPGLPSRVKCGSPGQLQGHSIFAQDLRLCLDETLSWNCFG

30 SEQ ID NO:7 (Porcine TLR9)

gagcacgaacatccttcactgtagctgctgcccggctctgccagccagaccctttggagaagacccccactccctgt
 catgggcccccgctgcacccctgcacccctttctctcctggctgcaggtgacagcgctggctgcccgtctggccca
 gggcaggtgctgccttctcctgcctgtgagctccagccccacggcctggtgaactgcaactggctcttctctgaa
 gtccgtgccccacttctcggcggcagcgccccgggccaacgtcaccagcctctccttactctccaaccgcatcca
 35 ccacctgcacgacttcgcacttcgctcactgtccagctcagcaactctcaacctcaagtggagtgcccccgggc
 tggcctcagccccatgcacttccccctgccatcagcattcgagcccaacaccttccctggcgtgcccacccctgga
 ggagctgaacctgagctacaacagcatcacgaccgtgctgcccactccctcgctgctcctgtcgctgag
 ccgcaccaacatcctggctgtagacccacccacctcactggcctacatgccctgcgctacctgtacatggatgg
 caactgctactacaagaacccctgccagggggcgctggaggtggtgcccgggtgccctcctcgccctgggcaacct
 40 cacacatctctcactcaagtaacaatctcacggaggtgccccgcagcctgccccccagcctggagacccctgct
 gttgtcctacaaccacattgtcacccctgacgctgaggacctggccaatctgactgccctgcgctgcttgatgt
 ggggggggaactgcccgcgctgtgaccatgcccgaacccctgcagggagtgcccaaaggaccaccccaagctgca
 ctctgacaccttcagccacctgagccgctcgaaggcctggtgttgaaagacagttctctctacaacctggacac
 caggtggttccgaggcctggacaggctccaagtgtgacacctgagtgagaacttccctctacgactgcatcacaa
 45 gaccacggccttcaggggcctggcccgactgcgagcctcaacctgtccttcaattaccacaagaaggtgtcctt
 tgccacctgacacctggcaccctcctttgggcacctccggctccctgaaggagctggacatgcatggcatcttctt
 ccgctcgctcagtgagaccacgctccaacctctggtccaactgcctatgctccagacccctgcgcctgcagatgaa
 cttcattaaccaggcccagctcagcatctttggggccttccctggcctgctgtacgtggacatcggaacaaccg
 catcagcggagctgcaaggccagtgccattactagggaggtggatggtagggagaggggtctggctgccttccag
 50 gaacctcgctccacgtccactggacactctccgctcagaggacttcatgccaaactgcaaggccttcagcttcac
 cttagacctgtctcggaacaacctggtgacaatccagtcggagatggttgctcgccctctcacgcctcgagtgcct
 ggcctgagccacaacagcatctccaggcggtcaatggctctcagtttgctgcgctgaccagcctgcgggtgct
 ggacgtgtcccaacaagctggacctgtatcacgggcgctcggttcacggagctgcccgcgctggaagcactgga
 cctcagctacaatagccagccctttaccatgcagggtgtggggccacaacctcagcttcgtggcccagctgcccgc

- 12 -

cctgcgctacctcagcctggcgacacatccatagccgagtggtcccagcagctctgtagcgccctcactgtg
cgccctggacttttagcggaacgatctgagccggatgtgggctgagggagacctctatctccgcttcttccaagg
cctaagaagccttagtctggctggacctgtcccagaaccacctgcacaccctcctgccacgtgccctggacaacct
5 ccccaaaagcctgaagcatctgcatctccgtgacaataacctggccttcttcaactggagcagcctgacctcct
gccaagctggaaacctggacttggctggaaaccagctgaaggccctaagcaatggcagcctgccatctggcac
ccagctgcggaggctggacctcagtggaacagcatcggtttgtgaacctggcttctttgccctggccaagca
gttagaagagctcaacctcagcgccaatgccctcaagacagtggagccctcctggtttggtcgtatgggtgggcaa
cctgaaagtccctagacgtgagcgccaacctctgcactgtgcctgtggggcgaccttcgtgggcttctgtctgga
10 ggtacaggctgccgtgcctgggctgccagccgcgtcaagtgtggcagtcggggcgacctccaggggccatagcat
ctttgcgcaagacctgcgctctgcctggatgagacctctcgtggaactgttttggtatctcgtgctggccat
ggcctgggctgggtgtgcccactgtgcacctctgcggctgggacctctggtactgcttccacctgtgcct
ggcctggctgccccaccgagggcagcgggcgagccctgttctatgatgccttcgtggtccttgacaa
agctcagagtgtgtggccgactgggtgtacaacagagctgcgggtgcagctggaggagcgccgtgggcgcgcgc
actgcgctgtgcctggaggagcgagactgggttacctggcaagacgtcttcgagaacctgtgggcctcagtcct
15 cagcagccgcaagacctgtttgtgctggccacacggacctgtcagcgccctcttgcgtgcagtttctgtct
ggccagcagcgctgtgaggaccgcaaggacgttgtagtgtggtgatcctgcgccccgatgcctaccgctc
ccgctacgtgcggctgcgccagcgctctgcgccagagtgtcctcctctggccccaccagccccgtgggcaggg
cagcttctggggccagctgggcacagccctgaccagggacaaccaccacttctataaccggaacttctgcgggg
ccccacgacagccgaatagcactgagtgcagccagttgccccagccccctggatttgctctctgctgggg
20 tgccccaacctgtcttgctcagccacaccactgtctgtcctgttccccacccccccccagcctggcatgt
aacatgtgccaataaatgtctaccggagggccaagaaaaaaaaaaaaaaaaaaaaa

SEQ ID NO:8 (Porcine TLR9)

atggggccccgctgcacctgcacccctttctctcctgggtgcaggtgacagcgctggctgcggctctggccag
25 ggcaggctgcctgccttctgcctgtgagctccagccccacggcctgggtgaactgcaactggctcttctgaag
tccgtgccccacttctcggcgagcgccccgggccaacgtcaccagcctctccttactctccaaccgcatccac
cacctgcacgactccgacttctccacctgtccagcctacgaactctcaacctcaagtggaaactgccccgggct
ggcctcagccccatgcacttccccctgccacatgaccatcgagcccaacaccttctggccgtgccaccctggag
gagctgaacctgagctacaacagcatcacgacctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcct
30 cgcaccaacatcctgggtgctagacccccaccacctcactggcctacatgcctgcctgcctgcctgcctgcct
aactgctactacaagaaccttgcagggggcgctggaggtgggtgcgggtgcctcctcgccctgggcaacctc
acacatctctcactcaagtacaacaatctcacggaggtgccccgcagcctgccccccagcctggagacctgtctg
ttgtcctacaaccacattgtcaccctgacgcctgaggacctggccaatctgactgcctgcctgcctgcctgcct
35 gggggggaactgccgctgtgacctgccccgaaccttgcagggagtgcccaaaggaccacccaagctgcac
tctgacaccttcagccacctgagccgctcgaaggcctgggtgtgaaagacagttctctctacaacctggacacc
aggtgggtcccgaggcctggacaggctccaagtgtggacctgagtgagaacttctctacgactgcacaccaag
accacggccttccaggcctggcccgactgcgcagcctcaacctgtccttcaattaccacaagaaggtgtccttt
gcccacctgcacctggcacctcctttgggcacctccggtccctgaaggagctggacatgcctggcatcttcttc
cgctcgctcagtgagaccacgtcccaacctctgggtccaaactgcctatgctccagacctgcgctgcagatgaac
40 ttcatataaccaggcccagctcagcatctttggggccttccctggcctgctgtacgtggacctatcggaacaaccg
atcagcggagctgcaaggccagtgccattactaggagggtggatggtagggagaggggtctggctgccttccagg
aacctcgctccacgtccactggacactctccgctcagaggacttcatgccaactgcaaggccttcagcttcacc
ttggacctgtctcggaacaacctgggtgacaatccagtcggagatgtttgtgcgctctcagcctcgagtgctg
45 cgctgagccacaacagcatctcccaggcggtcaatggctcctcagtttgctgcgctcagcctcgagtgctg
gacctgtcccacaacaagctggacctgtatcacggcgctcgttcacggagctgcgcgcctggaagcactggac
ctcagctacaatagccagccctttaccatgcagggtgtggggccacaacctcagcttcgtggccagctgcgcgc
ctgcgctacctcagcctggcgacacatgacatccatagccgagtgctccagcagctctgtagcgcctcactgtgc
gcctggacttttagcggaacgatctgagccggatgtgggctgagggagacctctatctccgcttcttccaaggc
ctaagaagcctagtctggctggacctgtcccagaaccacctgcacacctcctgccagctgcctggacaacctc
50 cccaaaagcctgaagcatctgcatctccgtgacaataacctggccttcttcaactggagcagcctgacctcctg
cccaagctggaaacctggacttggctggaaaccagctgaaggccctaagcaatggcagcctgccatctggcacc
cagctgcggaggctggacctcagtggaacagcatcggtttgtgaacctggcttctttgccctggccaagcag
ttagaagagctcaacctcagcgccaatgccctcaagacagtggagccctcctgggttggtcgtatgggtgggcaa
ctgaaagtccctagacgtgagcgccaacctctgcactgtgcctgtggggcgaccttcgtgggcttctgtctggag
55 gtacaggctgcgctgcctgggctgccagccgcgtcaagtgtggcagtcggggcgacctccaggggccatagcatc
tttgcgcaagacctgcgctctgcctggatgagacctctcgtggaactgttttggc

- 13 -

SEQ ID NO:9 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGLTLPALPCELQPHGQVDCNWLFLKSVPHFSAGAPRANVTSLSLISNRIH
 HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSL
 5 HTSILVLGPTHFTGLHALRFLYMDGNCYMNPCCPRALEVAPGALLGLGNLTHLSLKYNNLTEVPRRLPPSLDTLL
 LSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSLSRLEGLVLKDSSLYKLEK
 DWFRGLGRLQVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNYHKKVSAHLHLASSFGSLVSLEKLDMHGIF
 RSLTNITLQSLTRLPKLQSLHLQLNFINQAQLSIFGAFPSLLFVDLSDNRISGAATPAAALGEVDSRVEVWRLPR
 GLAPGPLDAVSSKDFMPSCNLTLDLNRNLTITQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD
 10 LSHNKL DLYHGRSFTELPQLEALDLSYNSQPFMSQGVGHNLSFVAQLPSLRYLSLAHNGIHSRVSQKLSSASLRA
 LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLDNLPKSLRQLRLRDNNLAFFNWSSLTVP
 RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIGFVRATRLIELNLSANALKTVDPSPWFGSLAGTL
 KILDVSANPLHCACGAAFVDFLLERQEAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLSDCFGLSLLMVA
 LGLAVPMLHHLCGWDLWYCFHLCLAHLPRRRRQRGEDTLLYDAVVVFDKVQSAVADWVYNELRVQLEERRRRAL
 15 RLCLEERDWLPKTLFENLWASVYSSRKTMTFVLDHTDRVSGLLRASFLLAQQRLEDRKDVVVLVILRPAAYRSR
 YVRLRQRLCRQSVLLWPHQPSGQGSFWANLGIALTRDNHRHFYNRNFCRGPTTAE

SEQ ID NO:10 (Bovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAEGLTLPALPCELQPHGQVDCNWLFLKSVPHFSAGAPRANVTSLSLISNRIH
 20 HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSL
 HTSILVLGPTHFTGLHALRFLYMDGNCYMNPCCPRALEVAPGALLGLGNLTHLSLKYNNLTEVPRRLPPSLDTLL
 LSYNHIVTLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSLSRLEGLVLKDSSLYKLEK
 DWFRGLGRLQVLDLSENFLYDYITKTTIFNDLTQLRRLNLSFNYHKKVSAHLHLASSFGSLVSLEKLDMHGIF
 RSLTNITLQSLTRLPKLQSLHLQLNFINQAQLSIFGAFPSLLFVDLSDNRISGAATPAAALGEVDSRVEVWRLPR
 25 GLAPGPLDAVSSKDFMPSCNLTLDLNRNLTITQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTSLRVLD
 LSHNKL DLYHGRSFTELPQLEALDLSYNSQPFMSQGVGHNLSFVAQLPSLRYLSLAHNGIHSRVSQKLSSASLRA
 LDFSGNSLSQMWAEGDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLDNLPKSLRQLRLRDNNLAFFNWSSLTVP
 RLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIGFVRATRLIELNLSANALKTVDPSPWFGSLAGTL
 KILDVSANPLHCACGAAFVDFLLERQEAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLSDCFGLSLLMVA
 30

SEQ ID NO:11 (Bovine TLR9)

gggaagtgggagcgaagcatccttccctgcagctgcctcccaacctgcccgcagaccctctggagaagccgcat
 tccctgtcatgggcccctactgtgccccgcaccccccttctctcctgggtgcaggcggcggcactggcagcggccc
 tggccgagggcaccctgcctgccttccctgcctgtgagctccagccccatgggtcaggtggactgcaactggctgt
 35 tccctgaagtctgtgcccgcacttttcggctggagccccccgggccaatgtcaccagcctctccttaattctccaacc
 gcatccaccacttgcatgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtggaaactgcc
 cgccggccggcctcagccccatgcacttccccctgcccgtatgaccatcgagcccaacaccttccctggctgtgccc
 ccctggaggagctgaacctgagctacaacggcatcacgaccgtgcctgcccgtgcccagttccctcgtgtccctgt
 cgctgagccacaccagcatcctgggtgctaggccccaccacttcaccggcctgcacgcccctgcgctttctgtaca
 40 tggacggcaactgctactacatgaaccctgcccgcgggcccctggaggtggcccagggcgcctcctcggcctgg
 gcaacctcacgcacctgtcgtcgaagtacaacaacctcacggaggtgccccgcgcctgccccccagcctggaca
 ccctgctgctgtcctacaaccacattgtcaccctggcaccggaggacctggccaacctgactgcccctgcgcgtgc
 ttgacgtgggtgggaactgccgcccgtgcgacctgcccgcgaaccttgcagggagtgcccaaagaacttcccca
 agctgcaccttgacaccttcagtcacctgagccgcccctcgaaggcctgggtgtgaaggacagttctctctacaaac
 45 tagagaaagattggttccgcggcctgggagggctccaagtgtcgacctgagtgagaacttccctctatgactaca
 tcaccaagaccacatcttcaacgacctgaccagctgcccagactcaacctgtccttcaattaccacaagaagg
 tgtccttcgcccacctgcacctagcgtcctccttgggagctcgtgtccctggagaagctggacatgcacggca
 tcttcttcgctccctcaccacatcacgctccagtcgctgaccggcgtgcccagctccagagctcgtcatctgc
 agctgaacttcacaaacggcccagctcagcatcttggggccttcccagcctgctcttcgtggacctgtcgg
 50 acaaccgcatcagcggagccgcgacgcccagcggcggcctggggggaggtggacagcagggtggaagtctggcga
 tgcccaggggcccctcgtccaggcccgtggacgcccgtcagctcaaaggacttcacgccaagctgcaacctcaact
 tcaccttgacctgtcacggaacaacctgggtgacaatccagcaagagatgtttaccgcctctcccgcctccagt
 gcctgcgcctgagccacaacagcatctcgcaggcgggttaatggctcccagttcgtgcccgtgaccagcctgcgag

- 14 -

tgctcgacctgtcccacaacaagctggacctgtaccatgggcgctcattcacggagctgccgcagctggaggcac
tggacctcagctacaacagccagcccttcagcatgcagggcgctgggccacaacctcagcttcgtggccagctgc
cctccctgcgctacctcagccttgccgcacaatggcatccacagccgctgtcacagaagctcagcagcgccctcgt
5 tgcgcgccttggaactcagcggcaactccctgagccagatgtgggcccagggagacctctatctctgctttttca
aaggcttgaggaacctgggtccagctggacctgtccgagaacctctgcacacctcctgctcgtcacctggaca
acctgcccagagcctgcggcagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgaccg
tcctgccccggctggaagccctggatctggcaggaaaccagctgaaggccctgagcaacggcagcctgccgcctg
gcatccggctccagaagctggacgtgagcagcaacagcatcggttcgtgatccccggcttcttcgtccgcgcga
ctcggtgatagagcttaacctcagcgccaatgccctgaagacagtggatccctcctgggttcggttccttagcag
10 ggacctgaaaatcctagacgtgagcgccaaccgcctccactgcgcctgcggggcgccctttgtggacttctgc
tggagagacaggaggccgtgccggggtgtccaggcgctcacatgtggcagtcggggccagctccaggggccga
gcatcttcacacaggacctgcgcctctgcttgatgagacctctccttggaactgctttggcctctcactgctaa
tgggtggcgctgggctggcagtgcccatgctgcaccacctctgtggctgggacctctggtactgcttcacctgt
gtctggccatttgccccgacggcgggcgagcgggcgaggacacctgctctatgatgccgtcgtgggtcttcg
15 acaaggtgcagatgacgtggctgattgggtgtacaacagactccgcgtgcagctggaggagcgccggggcgcc
ggcgctccgcctctgcctggaggagcagactgggtccctggtaagacgctcttcgagaacctgtgggcctcgg
tctacagcagccgcaagacctgttcgtgctggaccacacggaccgggtcagcgccctcctgcgcgcagcttcc
tgctggcccagcagcgctgttgaggaccgcaaggacgtcgtagtgctgggtgatcctgcgccccgcgcctatc
ggtcccgctacgtgcggctgcgccagcgctctgcgcagagcgctcctccttgggccccaccagcccagtgggc
20 agggtagtttctgggccaacctgggcatagccctgaccagggacaacctgacttctataaccggaacttctgcc
ggggccccacgacagccgaatagcacagagtgaactgcccag

SEQ ID NO:12 (Bovine TLR9)

atggggccctactgtgccccgcacccctttctctcctgggtgcaggcgggcgccactggcagcgccctggccgag
25 ggcacctgctgccttctcctgctgtgagctccagcccatgggtcaggtggactgcaactggctgttctgaag
tctgtgcccgcacttttcggctggagcccccgggccaatgtcaccagcctctccttaatctccaaccgcatccac
cacttgcatgactctgacttctcctcactgtccaacctgcgggtctcaacctcaagtggaaactgcccgcggcc
ggcctcagccccatgcacttccctgccgtatgaccatcgagcccaacaccttcttggtgtgcccaccctggag
gagctgaacctgagctacaacggcatcacgacctgcctgcccagttccctcgtgtccctgtcgctgagc
30 cacaccagcatcctgggtgctaggccccaccacttccacggcctgcacgcccctgcgcttctgtacatggacggc
aactgctactacatgaacccctgcccgcgggcccctggaggtggccccaggcgccctcctcggcctgggcaacctc
acgcacctgtcgctcaagtacaacaacctcacggaggtgccccgcgcctgccccccagcctggacacctgctg
ctgtcctacaaccacattgtcacctggcaccggaggacctggccaacctgactgccctgcgcgtgcttgacgtg
ggtgggaactgcgcgcgtgcgacctgcccgcacacctgcaggagtgcccaaagaacttccccaaagtgcac
35 cctgacaccttcagtcacctgagcgcctcgaaggcctgggtgtgaaggacagttctctctacaaactagagaaa
gattgggttcgcggcctgggcaggtccaagtgtcgacctgagtgagaacttctctatgactacatcaccaag
accaccatcttcaacgacctgaccagctgcgcagactcaacctgtccttcaattaccacaagaagggtgtccttc
gccacctgcacctagcgtcctccttgggagctcgtgtcctggagaagctggacatgcacggcatcttcttc
cgtccctcaccaacatcacgctccagtcgctgacctgggctgcccagctccagagctcgtatctgcagctgaac
40 ttcatcaaccaggcccagctcagcatcttggggccttcccagacctgctcttcgtggacctgtcggacaaccgc
atcagcggagccgcgacgccagcgccgcctgggggaggtggacagcaggggtggaagtctggcgattgcccagg
ggcctcgctccaggcccgtggacgcccgtcagctcaaaggacttcatgccaagctgcaacctcaacttcaccttg
gacctgtcacggaacaacctgggtgacaatccagcaagagatgtttaccgcctctcccgcctccagtgctgcgc
ctgagccacaacagcatctgcaggcggttaatggctcccagttcgtgcccgtgaccagcctgcgagtgctcgac
45 ctgtcccacaacaagctggacctgtacctggcgctcattcacggagctgcccagctggaggcactggacctc
agctacaacagccagcccttcagcatgcaggcgctggggccaacctcagcttcgtggcccagctgcctccctg
cgctacctcagccttgccgcacaatggcatccacagccgctgtcacagaagctcagcagcgcctcgttgccgcgc
ctggacttcagcggcaactccctgagccagatgtgggcccagggagacctctatctctgcttttcaaaggcttg
aggaacctgggtccagctggacctgtccgagaacctctgcacacctcctgcctcgtcacctggacaacctgccc
50 aagagcctgcggcagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgacctcctgccc
cggtggaagccctggatctggcaggaaaccagctgaaggccctgagcaacggcagcctgccgcctggcatccgg
ctccagaagctggacgtgagcagcaacagcatcggttcgtgatccccggcttcttcgtccgcgcgactcggtg
atagagcttaacctcagcgccaatgccctgaagacagtggatccctcctgggttcggttcccttagcaggggacctg
aaaatcctagacgtgagcgccaaccgcctccactgcgcctgcggggcgccctttgtggacttctgctggagaga
55 caggaggccgtgccggggtgtccaggcgctcacatgtggcagtcggggccagctccaggggccgacatcttc
acacaggacctgcgcctctgcctggatgagacctctccttggaactgctttggc

- 15 -

SEQ ID NO:13 (Equine TLR9)

MGPCHGALQPLSLLVQAAMLAVALAQGTLPFFLPCELQPHGLVNCNWFLKSVPHFSAAAPRDNVTSLSLLSNRI
 5 HHLHDSDFQAQLSNLQKLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNGITTPALPSSLVSLIL
 SRTNIIQLDPTSLTGLHALRFLYMDGNCYYKNPCGRALEVAPGALLGLGNLTHLSLKYNNTTTPRSLPPSLEYL
 LLSYNHIVTLAPEDLANLTALRVLDVGGNCRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSSLYQLN
 PRWFRGLGNLTVLDLSENFLYDCITKTKAFQGLAQLRRLNLSFNYHKKVSFAHLTLAPSFGLSLSLQELDMHGIF
 FRSLSQKTLQPLARLPMLQRLYLQMNFINQAQLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGGKKVWLTS
 10 RDLTPGPLDTPSSEDFMPSCKNLSFTLDLSRNNLVTVQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQV
 LDLSHNKLDLYHGSRFTELPRLEALDLSYNSQPFMRGVGHNL SFVAQLPTLRYLSLAHNGIHSRVSQQLCSTSL
 WALDFSGNSLSQMWAEGDLYLRFFQGLRSLIRLDLSQNRLHTLLPCTLGNLPKSLQLLRLRNNYLAFFNWSSLTL
 LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRSNII FVVPGFALATRLRELNLSANALRTEEPSWFGFLAG
 SLEVLVDVSANPLHCACGAAFVDFLLQVQAAPVGLPSRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFGSLV
 VALGLAMPMLHHLGCGDLWYCFHLGLAWLPRRGWQRGADALS YDAFVVDKAQSAVADWVYNELRVRLEERRGR
 15 ALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDQVSGLLRASFLLAQORLLEDKDVVVLVILSPDARR
 SRYVRLRQRLCRQSVLFWPHQPSGQRSFWAQLGMALTRDNRHFYNQNFRCGPTMAE

SEQ ID NO:14 (Equine TLR9)

MGPCHGALQPLSLLVQAAMLAVALAQGTLPFFLPCELQPHGLVNCNWFLKSVPHFSAAAPRDNVTSLSLLSNRI
 20 HHLHDSDFQAQLSNLQKLNKWNCPAGLSPMHFPCHMTIEPNTFLAVPTLEELNLSYNGITTPALPSSLVSLIL
 SRTNIIQLDPTSLTGLHALRFLYMDGNCYYKNPCGRALEVAPGALLGLGNLTHLSLKYNNTTTPRSLPPSLEYL
 LLSYNHIVTLAPEDLANLTALRVLDVGGNCRCDHARNPCVECPHKFPQLHSDTFSHLSRLEGLVLKDSSLYQLN
 PRWFRGLGNLTVLDLSENFLYDCITKTKAFQGLAQLRRLNLSFNYHKKVSFAHLTLAPSFGLSLSLQELDMHGIF
 FRSLSQKTLQPLARLPMLQRLYLQMNFINQAQLGIFKDFPGLRYIDLSDNRISGAVEPVATTGEVDGGKKVWLTS
 25 RDLTPGPLDTPSSEDFMPSCKNLSFTLDLSRNNLVTVQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQV
 LDLSHNKLDLYHGSRFTELPRLEALDLSYNSQPFMRGVGHNL SFVAQLPTLRYLSLAHNGIHSRVSQQLCSTSL
 WALDFSGNSLSQMWAEGDLYLRFFQGLRSLIRLDLSQNRLHTLLPCTLGNLPKSLQLLRLRNNYLAFFNWSSLTL
 LPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRSNII FVVPGFALATRLRELNLSANALRTEEPSWFGFLAG
 SLEVLVDVSANPLHCACGAAFVDFLLQVQAAPVGLPSRVKCGSPGQLQGRSIFAQDLRLCLDKSLSWDCFG
 30

SEQ ID NO:15 (Equine TLR9)

ctctgttctctgagctgttgccgcgtgaaggactgagcagacaaagcatcctcctctgcagctgctgccagtg
 tgccagctggaccctctggatcatctccactccctgtcatgggcccttgccatggtgccctgcagccctgtct
 ctctggtgcaggcggccatgctggccgtggctctggcccaaggcaccctgcctcccttctgcccgtgtgagctc
 35 cagccccacggcctggtgaactgcaactggctgttctgaagtccgtgccccacttctcagcagcagcaccgccg
 gacaatgtcaccagcctttctgtctccaaccgcatccaccacctccagcactccgactttgcccactgtcc
 aacctgcagaaactcaacctcaaatggaactgcccgcagccggcctcagccccatgcacttccccctgccacatg
 accatcgagcccaacactttctggctgtaccacccctggaggagctgaacctgagctacaacggcatcacgact
 gtgcctgcccctgcccagctccctctgtctccctgatcctgagccgcaccaacatcctgcagctagacccccaccagc
 40 ctacagggcctgcagctccctgcgcttctatacatggatggcaactgctactacaagaacccctgcgggcccggcc
 ctggagggtggccccaggcgccctccttggcctgggcaacctcaccacctgtcactcaagtacaacaacctcaca
 acggtgccccgcagcctgccccctagcctggagtacctgctgttctcctacaaccacattgtcaccctggcacct
 gaggacctggccaatctgactgccctgctgtgctcgatgtgggtggaaactgccgcccgtgtgacctgcacgc
 aaccctgctggagtggccacataaattccccagctgcactccgacaccttcagccacctaaagccgcctagaa
 45 ggccctgctgttgaaggatagttctctctaccagctgaacccagatggttccgtggcctgggcaacctcacagt
 ctgcacctgagtgagaacttctctacgactgcatcaccaaaaccaaggcattccagggcctggcccagctgcga
 agactcaacttgtccttcaattaccataagaagggtgtccttcgcccacctgacgctggcaccctccttcgggagc
 ctgctctccctgcaggaactggacatgcatggcatcttcttcgctcactcagccagaagacgctccagccactg
 gccgcctgcccagctccagcgtctgtatctgcagatgaacttcatcaaccaggcccagctcggcatcttcaag
 50 gacttccctgggtctgcgctacatagacctgtcagacaacccgcatcagtgaggctgtggagcgggtggccaccaca
 ggggaggtggatgggtgggaagaaggctgtggctgacatccaggacctcactccaggcccactggagacccccagc
 tctgaggacttcatgccaagctgcaagaacctcagcttccacttggacctgtcacggaacaacctggtaacagtc
 cagccagagatgtttgccagctctcgcgcctccagtgccctgcgctgagccacaacagcatctcgcaggcggctc

- 16 -

aatgggtcacagttcgtgccactgaccagcctgcaggtgctggacctgtcccataacaaactggacctgtaccat
gggcgctcggtttacggagctgccgcgactggaggccctggacctcagctacaacagccagcccttcagcatgcgg
ggtgtggggccacaacctcagctttgtggcccagctgccaccctgcgctacctcagcctggcacacaatggcatc
cacagccgtgtgtcccagcagctctgcagcacctcgctgtggggccctggacttcagcgggaattccctgagccag
5 atgtgggtgagggagacctctatctccgcttcttccaaggcctgagaagcctaataccggctagacctgtcccag
aatcgtctgcataacctcctgccatgcacctgggcaacctccccaagagcttgagctgctgcgtctccgtaac
aattacctggccttcttcaattggagcagcctgacctcctgcccaacctggaaacctggacctggctggaaac
cagctgaaggctctgagcaatggcagcctgccttctggcaccagctccagaggctggacgtcagcaggaacagc
atcatcttcgtggctccctggcttcttctgctctggccacgaggctgcgagagctcaacctcagtgccaacgcctc
10 aggacagaggagccctcctgggttgggttccctagcaggctcccttgaagtcctagatgtgagcgccaacctctg
cactgcgcctgtggggcagccttctgtgacttctcctgctgcaggttcaggctgcccgtgctggctgtgccagccgc
gtcaagtgtggcagtcggggcagctccaggggcgcagcatcttcgcacaagacctgcgcctctgctggacaag
tccctctcctgggactgttttgggtctctcattgtcgtggtgtggccctgggctggccatgcctatgttgaccac
ctctgcgcctgggacctctggtactgcttccacctgggctggcctggctgcccggcgggggtggcagcggggc
15 gcggtgcccctgagctatgatgccttctgtggtcttcgacaaggcacagagcgcagtgggcgactgggtgtacaat
gaactgcgggtgcggctagaggagcgcctggggcgccggcgctccgcctgtgtctggaggagcgtgactggcta
cctggcaagacgctgttcgaaaacctgtgggcctcagctacagcagccgcaagatgctgtttgtgctggccac
acggaccaggtcagtgccctcttgcgtgccagcttctcctgctggcccagcagcgtctgctggaggaccgcaaggac
gttgtggtgctggtaacctgagccctgacgcccgcggttcccggttacgtgcggctgcgccagcgcctctgccgc
20 cagagtgtcctcttctggccccaccagcctagtggccagcgcagcttctggggccagctaggcatggccctgacc
agggacaaccgccacttctataaccagaacttctgccggggcccgacgatggctgagtagcacagagtgcagcc
tggcatgtacaacccccagccctgaccttgctctctgcctatgatgccagctctgctcactctgtgacgcccc
tgctctgcctccgccacctcacccttgccatacagcaggcactcaataaatgccactggcaggccaaacagcca
aaaaaaaaaaaaaaaa

25

SEQ ID NO:16 (Equine TLR9)

atggggcccttgccatggtgccctgcagccctgtctcctgggtgcaggcgcccatgctggccgtggctctggcc
caaggcaccctgcctcccttccctgccctgtgagctccagccccacggcctgggtgaactgcaactggctgttctctg
aagtccgtgccccacttctcagcagcagcaccgccgggacaatgtcaccagcctttccttgctctccaaccgcatc
30 caccacctccacgactccgactttgcccaactgtccaacctgcagaaactcaacctcaaatggaactgcccgcca
gcccgcctcagccccatgcacttccctgccacatgacctcgagcccaacacttctcctggctgtaccacacctg
gaggagctgaacctgagctacaacggcatcacgactgtgcctgccctgccagctccctcgtgtccctgatcctg
agccgcaccaacatcctgcagctagacccaccagcctcacgggcctgcctgcccgtgcgcttctatacatggat
ggcaactgctactacaagaacctcgtggggcgggccctggagggtggccccaggcgccctccttggcctgggcaac
35 ctacccacctgtcactcaagtacaacaacctcacaacgggtgccccgcagcctgccccctagcctggagtacctg
ctggtgtcctacaaccacattgtcaccctggcacctgaggacctggccaatctgactgcccctgcgtgtgctcgat
gtgggtggaaactgccgcccgtgtgacctgcacgcaacctcgcgtggagtggccacataaatccccagctg
cactccgacaccttcagccacctaaagccgcctagaaggcctcggttggaaggatagttctctctaccagctgaac
cccagatgggttccgtggcctgggcaacctcacagtgtcgcacctgagtgagaacttccctctacgactgcatcacc
40 aaaaccaaggcatccagggcctggcccagctgcgaagactcaacttgtccttcaattaccataagaagggtgtcc
ttcgccacctgacgtggcacctccttcgggagcctgctctccctgcaggaaactggacatgcatggcatcttc
ttcgcctcactcagccagaagacgctccagccactggcccgcctgcccatgctccagcgtctgtatctgcagatg
aacttcatcaaccaggccagctcggcatcttcaaggacttccctgggtctgcgctacatagacctgtcagacaac
cgcatcagtggagctgtggagccgggtggccaccacaggggaggtggatgggtgggaagaaggctctggctgacatcc
45 agggacctcactccagggccactggacacccccagctctgaggacttcatgccaagctgcaagaacctcagcttc
accttggacctgtcacggaacaacctggttaacagctccagccagagatgtttgcccagctctcgcgcctccagtg
ctgcgcctgagccacaacagcatctcgaggcggtcaatggctcacagttcgtgccactgaccagcctgcaggtg
ctggacctgtcccataacaaactggacctgtaccatgggcgctcggttacggagctgcccgcgactggaggccctg
gacctcagctacaacagccagcccttcagcatgcggggtgtggggccacaacctcagcttcttggggccagctgccc
50 acctgcgctacctcagcctggcacacaatggcatccacagccgtgtgtccagcagctctgcagcacctcgctg
tggggccctggacttcagcggcaattccctgagccagatgtgggctgagggagacctctatctccgcttcttccaa
ggcctgagaagcctaataccggctagacctgtcccagaatcgtctgcataacctcctgccatgcacctgggcaac
ctccccaagagcttgagctgctgcgtctccgtaacaattacctggccttcttcaattggagcagcctgacctc
ctgcccacacctggaaacctggacctggctggaaaccagctgaaggctctgagcaatggcagcctgccttctggc
55 acccagctccagaggctggacgtcagcaggaacagcatcatcttcgtgggtccctggcttcttctgctctggccaag
aggctgcgagagctcaacctcagtgccaacgcctcaggacagaggagccctcctgggttgggttctcctagcaggc
tcccttgaagtcctagatgtgagcgccaacctctgcactgcgcctgtggggcagccttcttggacttccctgctg

- 17 -

cagggttcaggctgccgtgcctggtctgccagccgcgtcaagtgtggcagtcggggccagctccagggccgcagc
atcttcgcacaagacctgcgcctctgctggacaagtcctctcctgggactgttttgg

SEQ ID NO:17 (Ovine TLR9)

5 MGPYCAPHPLSLLVQAAALAAALAQGTLPAPFLPCELQPRGKVCNWLFLKSVPRFSAGAPRANVTSLSLISNRIH
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSL
RTSILVLGPTHFTGLHALRFLYMDGNCYKNPCQQAWEVAPGALLGLGNLTHLSLKYNLLEVPRLPPSLDTLL
LSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSSHLSRLEGLVLKDSSLYKLEK
10 DWFRGLGRLQVLDLSENFLYDYITKTTIFRNLTQLRRLNLSFNHYHKKVSFAHLQLAPSFGGLVSLKLDMHGIF
RSLTNTTLRPLTQLPKLQSLSLQNLFINQAEISIFGAFPSLLFVDLSDNRISGAARPVAALGEVDSGVEVWRWPR
GLAPGPLAAVSAKDFMPSCNLTLDLSDNNLVITIQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTRLRVLD
LSYNKLDLYHGRSFTLPLQLEALDLSYNSQPFMSQGVGHNLSFVAQLPSRLRYLSLAHNGIHSRVSQKLSSASLRA
LDFSGNSLSQMWAEGLDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLNLPKSLRQLRLRDNNLAFFNWSSTVLP
15 QLEALDLAGNQLKALSNGSLPPGTRLQKLDVSSNSIGFVTPGFFVLANRLKELNLSANALKTVDPFVFGRLTETL
NILDVSANPLHCACGAAFVDFLLEMQAAVPLSRRVTCGSPGQLQGRSIFAQDLRLCLDETSLDCFGFSLLMVA
LGLAVPMLHHLGWDLWYCFHLCLAHLPRRRRQRGEDTLLYDAFVVFDKAQSAVADWVYNELRVQLEERRRRAL
RLCLEERDWLPGKTLFENLWASVYSSRKTMFVLDHTDRVSGLLRASFLLAQQRLLEDKRDVVVLVILRPAAYRSR
YVRLRQLRCRQSVLLWPHQPSGQGSFWANLGMALTRDNRHFYNRNFCRGPTTAE

20 SEQ ID NO:18 (Ovine TLR9)

MGPYCAPHPLSLLVQAAALAAALAQGTLPAPFLPCELQPRGKVCNWLFLKSVPRFSAGAPRANVTSLSLISNRIH
HLHDSDFVHLSNLRVLNLKWNCPAGLSPMHFPCRMTIEPNTFLAVPTLEELNLSYNGITTVPALPSSLVSLSL
RTSILVLGPTHFTGLHALRFLYMDGNCYKNPCQQAWEVAPGALLGLGNLTHLSLKYNLLEVPRLPPSLDTLL
LSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKNFPKLHPDTFSSHLSRLEGLVLKDSSLYKLEK
25 DWFRGLGRLQVLDLSENFLYDYITKTTIFRNLTQLRRLNLSFNHYHKKVSFAHLQLAPSFGGLVSLKLDMHGIF
RSLTNTTLRPLTQLPKLQSLSLQNLFINQAEISIFGAFPSLLFVDLSDNRISGAARPVAALGEVDSGVEVWRWPR
GLAPGPLAAVSAKDFMPSCNLTLDLSDNNLVITIQEMFTRLSRLQCLRLSHNSISQAVNGSQFVPLTRLRVLD
LSYNKLDLYHGRSFTLPLQLEALDLSYNSQPFMSQGVGHNLSFVAQLPSRLRYLSLAHNGIHSRVSQKLSSASLRA
LDFSGNSLSQMWAEGLDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLNLPKSLRQLRLRDNNLAFFNWSSTVLP
30 QLEALDLAGNQLKALSNGSLPPGTRLQKLDVSSNSIGFVTPGFFVLANRLKELNLSANALKTVDPFVFGRLTETL
NILDVSANPLHCACGAAFVDFLLEMQAAVPLSRRVTCGSPGQLQGRSIFAQDLRLCLDETSLDCFG

SEQ ID NO:19 (Ovine TLR9)

gtcggcacgggaagtgcagcgcgaagcatccttccctgcagctgccgcccacttgcccgcagaccctctggaga
35 agccgcattccctgccatgggcccctactgtgccccgcaccccccttctctcctggtgcaggcggcgccgctggc
agcagccctggcccagggcaccctgcctgccttccctgcctgtgagctccagccccggggttaaggtgaactgcaa
ctggctgttctgaagtctgtgcccgccttttcggccggagccccccgggccaatgtcaccagcctctccttaat
ctccaaccgcatccaccacttgacgactctgacttcgtccacctgtccaacctgcgggtcctcaacctcaagtgc
40 gaactgcccgcggccggcctcagccccatgcacttccctgcccgcagcaccatcgagcccaacaccttccctggc
tgtgcccaccctggaggagctgaacctgagctacaatggcatcacgaccgtgcctgcccagttctctcgt
atccctgtcgtgagcgcaccagcatcctggtgctaggccccaccacttcaccggcctgcacgcccctgcgctt
tctgtacatggacggcaactgctactataagaaccctgccagcaggccgtggagggtggccccaggcgccctcct
tggcctgggcaacctcacgcacctgtcgtcaagtacaacaacctcacggagggtgccccgcgctgccccccag
cctggacacctgtcgtgtcctacaaccacatcatcaccctggcaccgcaggacctggccaatctgactgcct
45 gctgtgcttgatgtggcggaactgcccgcgctgcgaccacgcccgaacccctgcaggagtgcccaaagaa
cttccccaaagctgcacctgacaccttcagccacctgagccgctcgaaggcctggtgtgaaggacagttctct
ctacaaactagagaaagactggttccgcggcctgggcaggctccaagtgtcgacctgagtgagaacttccctcta
tgactacatcaccaagaccacctcttcaggaacctgaccagctgcgcagactcaacctgtccttcaattacca
caagaaggtgtccttcgcccacctgcaactggcaccctccttgggggctggtgtccctggagaagctggacat
50 gcacggcatccttctcgcctccctcaccaaccacgctccggcgctgaccagctgcccgaagctccagagctc
gagctgtcagctgaacttcatcaaccaggccgagctcagcatcttggggccttcccgagcctgctcttctgga
cctgtcggacaaccgcatcagcggagctgcgaggccggtggccgcccctcggggagggtggacagcggggtggaagt
ctggcggtggcccaggggcctcgtccaggcccgcgtggccgcccgtcagcgcgaaggacttcatgccaagctgcaa

- 18 -

cctcaacttcaccttggacctgtcacggaacaacctgggtgacgatccagcaggagatgtttacccgcctctccc
cctccagtgcctgcgccctgagccacaacagcatctcgcaggcggttaatggctcgcagttcgtgccgctgacccg
cctgcgagtgcctcgacctgtcctacaacaagctggacctgtaccatggcgctcggtcacggagctgccgcagct
5 ggaggcactggacctcagctacaacagccagcccttcagcatgcagggcgctggggccacaacctcagcttcgtggc
ccagctgccgtccctgcgctacctcagccttgcgcacaacggcatccacagccgcgtgtcacagaagctcagcag
cgctcgtcgcgcgacctggacttcagcggcaactccctgagccagatgtggggccgaggagacctctatctctg
cttcttcaaaggcttgaggaaacctgggtccagctggacctgtccaagaaccacctgcacacctcctgcctcgtca
cctggataacctgcccagagcctgcggcagctgcgtctccgggacaataacctggccttcttcaactggagcag
10 cctgactgttctgccccagctggaagccctggatctggcggaaccagctgaaggccctgagcaacggcagcct
gccacctggcaccggctccagaagctggacgtgagcagcaacagcatcggtttgtgaccttggtctcttctgt
ccttgccaaccggctgaagagcttaacctcagcgccaacgcctgaagacagtggatcccttctgggttcggtcg
cttaacagagacctgaatatcctagacgtgagcgccaacccgctccactgtgcctgcggggcggtcttctgtgga
cttctgtgctggagatgcaggcggtgcctgggtgtccaggcgctcacgtgtggcagtcggggcagctcca
15 gggccgcagcatcttcgcacaggacctgcgcctctgctggatgagacctctccttggtgactgcttgggtctct
gctgctaattgggtggcgctgggctggcggtgccatgctgcaccacctctgtggctgggacctgtggtactgctt
ccacctgtgtctggccatttgcggcagcgcggtggcgagcgggcgaggacacctgctctacgatgccttcgt
ggtcttcgacaaggcgcagagtgcagtgccgactgggtgtacaacagagctccgcgtgcagctggaggagcgccg
cgggcgccggcgctccgcctctgctggaggagcgagactggctccctggcaagacgctcttcgagaacctgtg
ggcctcggtctacagcagccgtaagacctgttcgtgctggaccacacggaccgggtcagtggtcctcctgcgcgc
20 cagcttctgctggcccagcagcgctgttgaggaccgcaaggatgtcgtggtgctggtgatcctgcgccccgc
cgctaccggtcccgctacgtgcggtgcgcagcgctctgcccagagcgctcctccttggtggccccaccagcc
cagtgggcagggtagcttctgggccaacctgggcatggcctgaccagggacaaccgccacttctataaccggaa
cttctgcccggggccccacgacagccgaatagcacagagtgactgcccag

25 SEQ ID NO:20 (Ovine TLR9)

atggggccctactgtgccccgaccccccttctctcctgggtgaggcggtggcgctggcagcagccctggcccag
ggcaccctgcctgccttctgcctgtgagctccagccccggggaagggtgaactgcaactggctgttctgaag
tctgtgcccgcgttttgcggcggagcccccgggccaatgtcaccagcctctccttaatctccaaccgcatccac
30 cacttgacgactctgacttgcctccacctgtccaacctgcgggtcctcaacctcaagtggaaactgccggccggcc
ggcctcagccccatgcacttcccctgcccgcagcatgaccatcgagcccaacaaccttctgggtgtgcccacctggag
gagctgaacctgagctacaatggcatcacgacctgcctgcccagttctctcgatccctgtcgctgagc
cgaccagcatcctgggtgctaggccccaccacttcaccggcctgcacgcctgcgtttctgtacatggacggc
aactgctactataagaaccttgcagcagggcgtggaggtggccccaggcgccctccttggtcctgggcaacctc
35 acgcacctgtcgctcaagtacaacaacctcacggaggtgccccgcgcctgccccccagcctggacacctgctg
ctgtcctacaaccacatcatcacctggcacccgaggacctggccaatctgactgcctgcgtgtgcttgatgtg
ggcgggaaactgccggcgtgcgaccacgcccgaaccttgcagggagtgcccaagaacttcccaagctgcac
cctgacaccttcagccacctgagccgcctcgaaggcctgggtgttgaggacagttctctctacaaactagagaaa
gactggttccgcggcctgggacggctccaagtgtcgcacctgagtgagaacttctctatgactacatcaccaag
40 accaccatcttcaggaacctgaccagctgcgcagactcaacctgtccttcaattaccacaagaagggtgtccttc
gccacctgcaactggcaccctccttgggggctgggtgtcctggagaagctggacatgcacggcatcttcttc
cgctccctcaccaacaccacgctccggcgctgaccagctgcccagctccagagctctgagctctgcagctgaac
ttcatcaaccaggccgagctcagcatcttggggccttcccagcctgctcttctgaggacctgtcggaacaaccgc
atcagcggagctgcgaggccggtggcgccctcggggaggtggacagcggggtggaagctcggcggtggccagg
45 ggcctcgctccaggccccgtggcgccgctcagcgcaaggacttcagccaagctgcaacctcaacttcaccttg
gacctgtcacggaacaacctgggtgacgatccagcaggagatgtttacccgcctctcccgcctccagtgctgcgc
ctgagccacaacagcatctcgcaggcggttaatggctcgcagttcgtgcccgtgacctgcgagtgctcgac
ctgtcctacaacaagctggacctgtaccatggcgctcggtcacggagctgcccagctggaggcactggacctc
agctacaacagccagcccttcagcatgcagggcggtggccacaacctcagcttcgtggcccagctgccgtccctg
50 cgctacctcagccttgcgcaacggcatccacagccgcgtgtcacagaagctcagcagcgctcgctgcgcgcc
ctggacttcagcggcaactccctgagccagatgtggggcgaggagacctctatctctgcttcttcaaaggcttg
aggaaacctgggtccagctggacctgtccaagaaccacctgcacacctcctgcctcgtcacctggataacctgcc
aagagcctgcggcagctgcgtctccgggacaataacctggccttcttcaactggagcagcctgactgttctgcc
cagctggaagccctggatctggcggaaccagctgaaggccctgagcaacggcagcctgccacctggcaccggg
ctccagaagctggacgtgagcagcaacagcatcggtttgtgaccttggttcttctgtccttgccaaccggctg
55 aaagagcttaacctcagcgccaacgcctgaagacagtggatcccttctggttcggctcgcttaacagagacctg
aatatcctagacgtgagcgccaacccgctccactgtgcctgcggggcggtcttctgaggacttctgctggagatg

- 19 -

caggcgccgtgcctgggctgtccaggcggtcacgtgtggcagtcggggccagctccaggggccgcagcatcttc
gcacaggacctgcgcctctgcctggatgagaccctctccttggactgctttggc

Complete nucleotide and amino acid sequences for canine and feline TLR9 are publicly available. For example, an amino acid sequence for canine TLR9 is available as GenBank accession number BAC65192 and its corresponding nucleotide sequence is available as GenBank accession number AB104899. An amino acid sequence for feline TLR9 is available as GenBank accession number AAN15751 and its corresponding nucleotide sequence is available as GenBank accession number AY137581.

Complete nucleotide and amino acid sequences for canine and feline TLR9 were also determined independently from those available from public databases.

An amino acid sequence of canine TLR9 is provided as SEQ ID NO:21. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:21 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of canine TLR9 (See Figure 1). Amino acids numbered 1-822 of SEQ ID NO:21 are presumptively extracellular domain and correspond to SEQ ID NO:22. SEQ ID NO:23 is a nucleotide sequence of canine TLR9 cDNA having an open reading frame corresponding to nucleotides 91-3186. SEQ ID NO:24 is a nucleotide sequence of canine cDNA encoding amino acids 1-822 of SEQ ID NO:21.

An amino acid sequence of feline TLR9 is provided as SEQ ID NO:25. Based on comparison with known amino acid sequences of human and murine TLR9, it appears that SEQ ID NO:25 includes sequence for at least a majority of the extracellular domain, all of the transmembrane domain, and at least a portion of the intracellular domain of feline TLR9 (See Figure 1). Amino acids numbered 1-820 of SEQ ID NO:25 are presumptively extracellular domain and correspond to SEQ ID NO:26. SEQ ID NO:27 is a nucleotide sequence of feline TLR9 cDNA having an open reading frame corresponding to nucleotides 87-3179. SEQ ID NO:28 is a nucleotide sequence of feline cDNA encoding amino acids 1-820 of SEQ ID NO:25.

SEQ ID NO:21 (Canine TLR9)

MGPCRGALHPLSLLVQAAALALALAQGTLPALPCELPQHLVNCNWLFLKSVPRFSAAAPRGNVTSLSLYSNRI
HHLHDYDFVHFVHLRRLNLKWNCPASLSPMHFPCHMTIEPNTFLAVPTLEDNLNSYNSITTVPALPSSLVLSL
SRTNILVLDPATLAGLYALRFLFDGNCYYKNPCQALQVAPGALLGLGNLTHLSLKYNNTTVVPRGLPPSLEYL

- 20 -

LLSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKGFPPQLHPNTFGHLSHLEGLVLRDSSLYSLD
 PRWFHGLGNLMVLDLSENFLYDCITKTKAFYGLARLRRLNLSFNYHKKVSFAHLHLASSFGSLLSLQELDIHGIF
 FRSLSKTTLQSLAHLPLMLQRLHLQNLNFISSQAQLSIFGAFFPGLRYVDLSNDRISGAAPAAATGEVEADCGERVWP
 QSRDLALGPLGTPGSEAFMPSCRTLNFTLDLSRNNLVTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL
 5 RVLDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFMRGVGHNLVSFAQLPALRYLSLAHNGIHSRVSQQLRSA
 SLRALDFSGNTLSQMWAEGDLYLRFFQGLRSLVQLDLSQNRLHTLLPRNLDNLPKSLRLLRLRDNYLAFFNWSSL
 ALLPKLEALDLAGNQLKALSNGSLPNGTQLQRLDLSGNSIGFVVPSFFALAVRLRELNLSANALKTVEPSWFGSL
 AGALKVLDVTANPLHCACGATFVDFLLEVQAAVPGPLSRVKCGSPGQLQGRSIFAQDLRLCLDEALSWVCFSLSL
 LAVALSLAVPMLHQLCGWDLWYCFHLCLAWLPRRGRRGVDALAYDAFVVDKAQSSVADWVYNELRVQLEERRG
 10 RRALRLCLEERDWPVKTLFENLWASVYSSRKTFLVLARTDRVSGLLRASFLLAQQRLLLEDKDVVVLVILCPDA
 HRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGTALTRDNRHFYNQNFRCGPTTA

SEQ ID NO:22 (Canine TLR9)

MGPCRGALHPLSLLVQAAALALALAQGTLPAPFLPCELQPHGLVNCNWLFLKSVPRFSAAAPRGNVTSLSLYSNRI
 15 HHLHDYDFVHFVHLRRLNLKWNCPASLSPMHFPCHMTIEPNTFLAVPTLEDNLNSYNSITTVPALPSSLVSLSL
 SRTNIIVLDPATLAGLYALRFLFDGNCYKNPCQQALQVAPGALLGLGNLTHLSLKYNNTLVVPRGLPPSLEYL
 LLSYNHIITLAPEDLANLTALRVLDVGGNCRRCDHARNPCRECPKGFPPQLHPNTFGHLSHLEGLVLRDSSLYSLD
 PRWFHGLGNLMVLDLSENFLYDCITKTKAFYGLARLRRLNLSFNYHKKVSFAHLHLASSFGSLLSLQELDIHGIF
 FRSLSKTTLQSLAHLPLMLQRLHLQNLNFISSQAQLSIFGAFFPGLRYVDLSNDRISGAAPAAATGEVEADCGERVWP
 20 QSRDLALGPLGTPGSEAFMPSCRTLNFTLDLSRNNLVTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNL
 RVLDLSHNKLDLYHGRSFTELPRLEALDLSYNSQPFMRGVGHNLVSFAQLPALRYLSLAHNGIHSRVSQQLRSA
 SLRALDFSGNTLSQMWAEGDLYLRFFQGLRSLVQLDLSQNRLHTLLPRNLDNLPKSLRLLRLRDNYLAFFNWSSL
 ALLPKLEALDLAGNQLKALSNGSLPNGTQLQRLDLSGNSIGFVVPSFFALAVRLRELNLSANALKTVEPSWFGSL
 AGALKVLDVTANPLHCACGATFVDFLLEVQAAVPGPLSRVKCGSPGQLQGRSIFAQDLRLCLDEALSWVCFSS

SEQ ID NO:23 (Canine TLR9)

aggaaggggctgtgagctccaagcatcctttcctgcagctgctgcccagcctgccagccagaccctctggagaag
 ccccgctccctgtcatgggccccctgccgtggcgccctgcacccccctgtctctcctgggtgcaggctgccgcgcta
 gccctggccccctggccccagggcaccctgcctgccttccctgccctgtgagctccagccccatggcctgggtgaactgc
 30 aactggctgttccctcaagtcctgccccgcttctcggcagctgcacccccgggtaacgtcaccagccttcccttg
 tactccaaccgcatccaccacctccatgactatgactttgtccacttcgtccacctgcggcgctctcaatctcaag
 tggaaactgccccgccccgagcctcagccccatgcactttccctgtcacatgaccattgagcccaacaccttccctg
 gctgtgccccaccctagaggacctgaatctgagctataacagcatcacgactgtgccccccctgccagttcgctt
 gtgtccctgtccctgagcgcaccaacatcctgggtgctggaccctgccaccctggcaggcctttatgccctgcgc
 35 ttccctgttccctggatggcaactgctactacaagaacccctgccagcaggccctgcagggtggccccaggtgccctc
 ctgggcctgggcaacctcacacacctgtcactcaagtaacaacacctcacctgggtgcccggggcctgcccccc
 agcctggagtagctgtccttctcctacaaccacatcacctggcaccctgaggacctggccaatctgactgcc
 ctgcgtgtcctcgatgtgggtgggaactgtcgccgctgtgaccatgcccgtaacccctgcaggaggtgccccaa
 ggcttccccagctgcacccaacaccttcggccacctgagccacctcgaaggcctgggtgtgagggaacagctct
 40 ctctacagcctggacccccaggtggttccatggcctgggcaacctcatggtgctggacctgagtgagaacttccctg
 tatgactgcatcaccaaaaccaaagccttctacggcctggccccgctgcgcagactcaacctgtccttcaattat
 cataagaaggtgtcctttgccacctgcatctggcatcctccttcgggagcctactgtccctgcaggagctggac
 atacatggcatcttctccgctcgctcagcaagaccacgctccagtcgctggccccacctgccatgctccagcgt
 ctgcatctgcagttgaactttatcagccaggccagctcagcatcttcggcgccctccctggactgcggtagctg
 45 gactgtcagacaaccgcatcagtgagctgcagagcccgcggtgccacaggggaggtagaggcagactgtggg
 gagagagtctggccacagtcggggaccttgctctggggccactggggcaccctcggtcagaggccttcatgccg
 agctgcaggaccctcaacttcaccttgacctgtctcggaacaacctagtactgttcagccggagatgtttgtc
 cggtggcgcgccctccagtgccctgggcctgagccacaacagcatctcgaggcggtcaatggctcgcagttcggtg
 cctctgagcaacctgcgggtgctggacctgtcccataacaagctggacctgtaccacggggcgctcggttcacggag
 50 ctgcccgcggtggaggccttgacctcagctacaacagccagcccttcagcatgcggggcggtggggccacaatctc
 agctttgtggcacagctgccagccctgcgctacctcagcctggcgcaaatggcatccacagcccgctgtcccag
 cagctccgcagcgccctcgctccgggccccctggacttcagtggaataacccctgagccagatgtgggcccaggaggac
 ctctatctccgcttcttccaaggcctgagaagcctgggttcagctggacctgtcccagaatcgctgcataccctc
 ctgccacgcaacctggacaacctccccaaagcctgcggctcctgcggctccgtgacaattacctggcttctctc
 55 aactggagcagcctggccctcctaccaagctggaagcctggacctggcgggaaaccagctgaagggccctgagc

- 21 -

aatggcagcttgcccaacggcaccagctccagaggctggacctcagcggcaacagcatcggcttcgtggtcccc
 agcttttttgccttgccgtgaggttcgagagctcaacctcagcggcaacgccctcaagacgggtggagccctcc
 tggtttgggtccctggcgggtgacctgaaagtccctagacgtgacggccaaccccttgcatcgtcgtgaggcgca
 5 accttcgtggacttcttgctggaggtgcaggctgagggtgcccggcctgcctagccgtgtcaagtgcggcagcccg
 ggccagctccaggggccgcagcatcttcgcacaggacctgcgcctctgcctggacgaagcgctctcctgggtctgt
 ttcagacctctcgtgctggtgctggtgacctgacctggtgctgacctgacctgacctgacctgacctgacctg
 tggtagctgcttccacctgctgacctgacctgacctgacctgacctgacctgacctgacctgacctgacctg
 gacgacctcgtggtcttcgacaaggcgagagctcgggtggcggaactgggtgtacaatgagctgcgggtacagcta
 10 gaggagcgccgtggcgccggcgctacgacctgtgtctggaggaaactgactgggtacccggcaaaacctcttc
 gagaacctctgggacctcagtttacagcagccgcaagacgctgtttgtgctggcccgacggacagagtgcgggc
 ctctgctgctgacgcttctcgtgctggcccaacagcgctgctggaggaccgcaaggacgctcgtggtgctggtgatc
 ctgtgccccgacgcccaccgctcccgctatgtgctggctgcccagcgctctgcccagagctgctcctcctctgg
 cccaccagccagtggtggcagcgagcttctgggcccagctgggacggccctgaccagggacaaccgcccacttc
 tacaaccagaacttctgcccggggccccacgacagcctgataggcagacagcccagcaccttcgcccctacacc
 15 ctgacctgtctgtctgggatgcccagacctgctggtctacaccgcccgtctgtctcccctacaccagccctggca
 taaagcgaccgctcaataaatgctgctggtgagac

SEQ ID NO:24 (Canine TLR9)

atgggccccctgcccgtggcgccctgcacccccctgtctctcctgggtgcaggctgccgcgctagccctggccctggcc
 20 cagggcaccctgacctgaccttccctgacctgtgagctccagccccatggcctgggtgaactgcaactggctgttccctc
 aagtccgtgccccgcttctcggcagctgcacccccgggtaacgtcaccagcctttccttgtagtccaaccgcatc
 caccacctccatgactatgactttgtccacttcgtccacctgcccgtctcaatctcaagtggaaactgcccggcc
 gccagcctcagccccatgcactttccctgtcacatgaccattgagcccaacaccttccctggctgtgcccacccta
 gaggacctgaatctgagctataacagcatcacgactgtgcccgcctgcccagttcgttgtgtccctgtccctg
 25 agccgcaccaacatcctgggtgctggacctgcccacctggcaggcctttatgcccctgcgcttccctgttccctggat
 ggcaactgctactacaagaacccctgccagcaggccctgcagggtggccccagggtgcctcctgggctgggcaac
 ctcacacacctgtcactcaagtacaacaacctcaccgtgggtgcccggggcctgccccaggtgcctcctgggctgggcaac
 ctcttctcctacaaccacatcatcaccctggcacctgaggacctggccaatctgactgacctgacctgacctgacctg
 gtgggtgggaactgtgcccgtgtgacctgcccgttaacccctgcaggagtgccccagggttccccagctg
 30 ccccccaacaccttggccacctgagccacctcgaaggcctgggtgttgaggagacagctctctctacagcctggac
 cccaggtgggttccatggcctgggcaacctcatgggtgctggacctgagtgagaacttccctgtatgactgcatcacc
 aaaaccaaaagccttctacggcctggcccgggtgcccagactcaacctgtccttcaattatcataagaagggtgtcc
 tttgcccacctgcatctggcatctccttccgggagcctactgtccctgcaggagctggacatacatggcatcttc
 ttccgctcgtcagcaagaccagctccagtcgctggcccacctgcccagctccagcgtctgcatctgcagttg
 35 aactttatcagccaggcccagctcagcatcttcggcgcccttccctggactgcgggtacgtggacttgtcagacaac
 cgcacagtgaggctgcagagcccgcggctgccacaggggaggttagaggcagactgtggggagagagctctggcca
 cagtcccgggaccttgccttggggccactgggcacccccggctcagaggccttcatgccgagctgcaggacctc
 aacttcaccttgacctgtctcggaacaacctagtactgttcagccggagatgtttgtccggctggcgcgccctc
 cagtgcctgggctgagccacaacagcatctcgcaggcgggtcaatggctcgcagttcgtgcctctgagcaacctg
 40 cgggtgctggacctgtcccataacaagctggacctgtaccacggggcgtcggtcacaggagctgcccgggctggag
 gccttgacctcagctacaacagccagcccttcagcatgcggggcgtgggcccacaatctcagctttgtggcacag
 ctgccagccctgcgctacctcagcctggcgccacaatggcatccacagccgcgtgtcccagcagctccgcagcgcc
 togtccggggccttgacttcagtggcaataacctgagccagatgtgggcccaggaggagacctctatctccgcttc
 ttccaaggcctgagaagcctgggtcagctggacctgtcccagaatcgccctgcataacctcctgccacgcaacctg
 45 gacaacctccccaaagagcctgcggctcctgcggctccgtgacaattacctggctttcttcaactggagcagcctg
 gccctcctacccaagctggaagccctggacctggcgggaaaccagctgaaggccctgagcaatggcagcttgccc
 aacggcacccagctccagaggctggacctcagcggcaacagcatcggttcgtgggtccccagcttttttgccttg
 gccgtgaggcttcgagagctcaacctcagcggcaacgcctcaagacgggtggagccctcctgggtttgggtccctg
 gcgggtgacctgaaagtccctagacgtgaccgccaaccccttgcatcgtctgcggcgcaaccttcgtggacttc
 50 ttgctggagggtgcaggctgcgggtgcccggcctgacctagccgtgtcaagtgcggcagccccgggcccagctccagggc
 cgcagcatcttcgcacaggacctgcgcctctgacctggacgaagcgctctcctgggtctgtttcagc

SEQ ID NO:25 (Feline TLR9)

55 MGPCHGALHPLSLLVQAAALAVALAQGTLPALFLPCELQRHGLVNCDWLFLKSVPHFSAAAPRGNVTSLSLSYNSRI
 HHLHDSDFVHLSSLRLNLKWNCPASLSPMHFPCHMTIEPHTFLAVPTLEELNLSYNSITTVPALPSSLVSLSL

- 22 -

SRTNIVLDPANLAGLHSLRFLFDGNCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYL
 LLSYNHIIITLAPEDLANLTALRVLDVGGNCRCDHARNPCMECPKGFPHLHPDTFSLNHLEGLVLKDSSLYNLN
 PRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRRLNLSFNHKKVSFAHLHLAPSFGLSLSLQQLDMHGIF
 FRSLSETTLRSLVHLPMLQSLHLQMNFINQAQLSIFGAFPLGRYVDLSDNRISGAMELAAATGEVDGGERVRLPS
 5 GDLALGPPGTPSSEGFMPGCKTLNFTLDLSRNNLVITIQEMFARLSRLQCLLSRNSISQAVNGSQFMPLTSLQV
 LDLSHNKLDLYHGRSFTLPRLEALDLSYNSQPFMSMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSASL
 RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNRLHTLLPRTLNDLPKSLRLLRLRDNYLAFFNWSSSLVL
 LPRLEALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVASSFFALATRLRELNLSANALKTVEPSWFGSLAG
 10 TLKVLVDVTGNPLHCACGAADFVDFLLEVQAAVPGPLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDGFLSLLT
 VALGLAVPMLHHLGWDLYWCFHLCLAWLPRRGRRGADALPYDAFVVDKAQSAVADWVYNELRVRLREERRGR
 ALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDRVSGLLRASFLLAQQRLLLEDKDVVVLVILRPDAHR
 SRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGTALTRDNQHFYNQNFRCGPTTAE

SEQ ID NO:26 (Feline TLR9)

15 MGPCHGALHPLSLIVQAAALAVALAQGTLPAPFLPCELQRHGLVNCDWLFLKSVPHFSAAAPRGNVTLSLSYNNRI
 HHLHDSDFVHLSSLRRLNLKWNCPASLSPMHFPCMTIEPHTFLAVPTLEELNLSYNSITTVPALPSSLSVLSL
 SRTNIVLDPANLAGLHSLRFLFDGNCYYKNPCPQALQVAPGALLGLGNLTHLSLKYNNTAVPRGLPPSLEYL
 LLSYNHIIITLAPEDLANLTALRVLDVGGNCRCDHARNPCMECPKGFPHLHPDTFSLNHLEGLVLKDSSLYNLN
 20 PRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRRLNLSFNHKKVSFAHLHLAPSFGLSLSLQQLDMHGIF
 FRSLSETTLRSLVHLPMLQSLHLQMNFINQAQLSIFGAFPLGRYVDLSDNRISGAMELAAATGEVDGGERVRLPS
 GDLALGPPGTPSSEGFMPGCKTLNFTLDLSRNNLVITIQEMFARLSRLQCLLSRNSISQAVNGSQFMPLTSLQV
 LDLSHNKLDLYHGRSFTLPRLEALDLSYNSQPFMSMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCSASL
 RALDFSGNALSRMWAEGDLYLHFFRGLRSLVRLDLSQNRLHTLLPRTLNDLPKSLRLLRLRDNYLAFFNWSSSLVL
 LPRLEALDLAGNQLKALSNGSLPNGTQLQRLDLSNSISFVASSFFALATRLRELNLSANALKTVEPSWFGSLAG
 25 TLKVLVDVTGNPLHCACGAADFVDFLLEVQAAVPGPLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDGFG

SEQ ID NO:27 (Feline TLR9)

agggctctgcgagctccaggcattcttctctgcatcgctgccagctctgcatccagaccctctggagaagcccc
 cactccctgtcatgggcccctgcatggcgccctgcaccccctgtctctctggtgcaggctgccgcgctggccg
 30 tggccctggcccagggcaccctgcctgcttctgcccctgtgagctccagcgccacggcctggtgaattgcgact
 ggctgttccctcaagtccgtgccccacttctcgccggcagcgccccctggttaacgtcaccagcctttccctgtact
 ccaaccgcatccaccacctccagcactccgacttctgtccacctgtccagcctgcggcgtctcaacctcaaatgga
 actgcccacccgcccagcctcagccccatgcacttcccctgtcacatgaccattgagccccacaccttccctggccg
 tgcccacccctggaggagctgaacctgagctacaacagcatcacgacagtaccggccctgccaggttccctcgtgt
 35 cctgtccttgagccgtaccaacatcctggtgctggaccctgccaacctgcagggtgcactccctgcgcttct
 tgttccctggatggcaactgctactacaagaacccctgcccgcaggccctgcagggtggccccggcgccctccttg
 gcctgggcaaccttacgcacctgtcactcaagtacaacaacctcactgcggtgccccgcggcctgccccccagcc
 tggagtacctgctattgtcctacaaccacatcatcaccctggcacctgaggacctggccaacctgaccgcccctgc
 gtgtgctcgatgtgggtgggaactgcctgcgtgtgaccacgcccgaacccctgtatggagtgccccaaagggt
 40 tcccgccactgcaccctgacaccttcagccacctgaaccacctgaaggcctggtgtgaaggacagctctctct
 acaacctgaaccccagatgggttccatgccctggggaacctcatggtgctggacctgagtgagaacttccatatatg
 actgcatcaccaaaaccacagccttccaggccctggcccagctgcgcagactcaacttgtcttccaattaccaca
 agaagggtgtcctttgcccacctgcatctggcgccctccttcgggagcctgctctccctgcagcagctggacatgc
 atggcatcttcttccgctcgctcagcgagaccacgctccggtcgctgggtccacctgcccagctccagagctctgc
 45 acctgcagatgaacttcatcaatcaggcccagctcagcatcttcggggccttccctggcctgcgatacgtggacc
 tgtcagacaaccgcataagtggagccatggagctggcggtgccacgggggaggtggatgggtggggagagagtcc
 ggctgccatctggggacctagctctggggccaccgggcacccctagctccgagggttcatgccaggctgcaaga
 ccctcaacttcaacttggacctgtcacggaacaacctagtgacaatccagccagagatgtttgcccggctctcgc
 gcctccagtgctgctcctgagccgcaacagcatctcgcaggcagtcacaggctcacaatttatgccgctgacca
 50 gcctgcagggtgctggacctgtcccataacaagctggacctgtaccatgggctcttccacggagctgccgcggc
 tggaggccctggacctcagctacaacagccagcccttcagcatgcaggcgctgggtcacaacctcagcttctgtgg
 cacagctgccggccctgcgctatctcagcctggcgcaacgacatccacagccgtgtgtcccagcagctctgca
 gcgctcgctgcgggccttggaacttcagcggcaatgccttgagccgatgtgggcccaggaggagacctgtatctcc
 acttcttccgaggcctgaggagcctgggtccggttgatctgtccagaatcgccctgcataccctcttgccacgca
 55 ccttggaacaacctccccaaagagcctgcggctgctgcgctctccgtgacaattatctggcttcttcaactggagca

- 23 -

gcctggctcctcctccccaggctggaagccctggacctggcggaaccagctgaaggccctgagcaacggcagct
 tgctaataaggaaccagctccagaggctggacctcagcagcaacagtatcagcttcgtggcctccagcttttttg
 ctctggccaccaggctgcgagagctcaacctcagtgccaacgcctcaagacgggtggagccctcctgggttcggtt
 5 ctctagcgggacacctgaaagtccatagatgtgactggcaacccctgcaactgcgcctgtggggcggccttcgtgg
 acttcttgctggaggtgcaggctgcagtgcccggcctgcccaggccacgtcaagtgtggcagtcagggtcagctcc
 agggccgcagcatctttgcgaggatctgcgcctctgctggatgaggccctctcctgggactgttttggcctct
 cgctgctgaccgtggcctggcctggcctggcctgcccagctgcaccacctctgtggctgggacctctggtactgct
 tccacctgtgctggcctggcctggcctggcctggcctggcctggcctggcctggcctggcctggcctggcctggcct
 10 tggctctcgacaaggcacagagcgcggtggcgcactgggtgtacaacgagctgcgggtacggctagaggagcgcc
 gtggacgcccagcgctccgcctgtgctggaggaaactgactggctacccggtaaaacgctctttgagaacctgt
 gggcctcagtttacagcagccgcaagatgctgtttgtgctggcccacacagacagggtcagcggcctcttgcgcg
 ccagctttctgctggccagcagcgctgctggaggaccgcaaggacgttgtggtgctggtgatcctgcgccccg
 acgcccaccgctcccgctatgtgcggctgcgcccagcgctctgcgcccagagcgctcctcctctggccccaccagc
 ccagtggccagcgagcctctggggccagctgggcacggccctgaccagggaaccagcacttctataaccaga
 15 acttctgcccggggccccacgacggcagagtgaccgcccagcaccccaagcctcctacaccttgctgtctgctg
 ggatgcccggg

SEQ ID NO:28 (Feline TLR9)

atgggcccctgccaatggcgccctgcacccctgtctctcctgggtgcaggctgcccgcgtggccgtggccctggcc
 20 cagggcaccctgctgctttctgcctgtgagctccagcgcacggcctgggtgaattgcgactggctgttcctc
 aagtccgtgccccacttctcgcgccagcgcgcctggtaacgtcaccagccttccctgtactccaaccgcac
 caccacctccagcactccgactttgtccacctgtccagcctgcccgcgtctcaacctcaaatggaactgccaccc
 gccagcctcagccccatgcacttccctgtcacatgaccattgagccccacaccttccctggcgtgcccacccctg
 gaggagctgaacctgagctacaacagcatcacgacagtaccgcctgcccagttccctcgtgtccctgtccttg
 25 agcgtaccacacatcctgggtgctggacctgccaacctgcagggtgactcctcgtccttctgttccctggat
 ggcaactgctactacaagaacctgcccgcaggccctgcagggtggccccggcgccctccttggcctgggcaac
 cttacgcacctgtcactcaagtacaacaacctcactgcgggtgccccggcctgccccccagcctggagtagctg
 ctattgtcctacaaccacatcatcacctggcacctgaggacctggccaacctgaccgcccgtgctgtgctgag
 gtgggtgggaactgcccgtcgctgtgaccacgcccgaacctctgtatggagtggcccaagggtctcccgacctg
 30 caccctgacaccttcagccacctgaaccacctgaaggcctgggtgttgaggacagctctctctacaacctgaac
 ccagatgggtccatgcccctgggcaacctcatgggtgctggacctgagtgagaacttccatatactgactgcacac
 aaaaccacagccttccaggccctggcccagctgcgcagactcaacttgtctttcaattaccacaagaagggtgtcc
 tttgcccacctgcatctggcgccctccttcgggagcctgctctccctgcagcagctggacatgcatggcatcttc
 ttcgctcgtcagcgagaccagctccggtcgctgggtccacctgcccagctccagagctctgcacctgcagatg
 35 aacttcatcaatcaggcccagctcagcatcttcggggccttccctggcctgcgatacgtggacctgtcagacaac
 cgcataagtggagccatggagctggcggtgcccaggggaggtggatgggtgggagagagctccggctgccatct
 ggggacctagctctggggccaccgggcaacctagctccgagggcttcatgccaggctgcaagacctcaacttc
 accttggacctgtcacggaacaacctagtgcacatccagccagagatgtttgcccggctctcgcgccctccagtgc
 ctgctcctgagccgcaacagcatctcgagggcagtcacggctcacaatttatgcccgtgaccagcctgcagggtg
 40 ctggacctgtcccataacaagctggacctgtaccatggcgctctttcacggagctgcccgggctggaggccctg
 gacctcagctacaacagccagcccttcagcatgcaggcgctgggtcacaacctcagctttgtggcacagctgccc
 gccctgcgctatctcagcctggcgcaacaacgacatccacagccgtgtgtcccagcagctctgcagcgcctcgctg
 cgggccttggacttcagcggcaatgccttgagccgatgtgggcccaggagagacctgtatctccacttcttcga
 ggctgaggagcctgggtccgggtggatctgtcccagaatcgctgcataacctcttgccacgcacctggacaac
 45 ctcaccaagagcctgcggctgctgcgtctccgtgacaattatctggctttcttcaactggagcagcctggctctc
 ctcccaggttgaagccctggacctggcgggaaaccagctgaaggccctgagcaacggcagcttgccataatgga
 accagctccagaggctggacctcagcagcaacagtatcagcttcgtggcctcagctttttgtctctggccacc
 aggtgagagagctcaacctcagtgccaacgcctcaagacgggtggagccctcctggttcgtctctagcgggc
 acctgaaagtccatagatgtgactggcaacccctgcaactgcgcctgtggggcgccctcctggtgacttctgctg
 50 gaggtgcaggctgcagtgcccggcctgcccaggccacgtcaagtgtggcagtcagggtcagctccaggcccgagc
 atctttgcgaggatctgcgcctctgctggatgaggccctctcctgggactgttttggc

Complete nucleotide and amino acid sequences for murine and human TLR9 are publicly available. For example, an amino acid sequence of murine TLR9 is available as

- 24 -

GenBank accession no. AAK29625, provided as SEQ ID NO:29. Amino acids numbered 1-821 of SEQ ID NO:29 presumptively include the entire extracellular domain and correspond to SEQ ID NO:30. SEQ ID NO:31 corresponds to GenBank accession number AF348140, which is a nucleotide sequence of murine TLR9 cDNA. SEQ ID NO:32 is a nucleotide
 5 sequence of murine cDNA encoding amino acids 1-821 of SEQ ID NO:29.

An amino acid sequence of human TLR9 is available as GenBank accession no. AAF78037, provided as SEQ ID NO:33. Amino acids numbered 1-820 of SEQ ID NO:33 presumptively include the entire extracellular domain and correspond to SEQ ID NO:34. SEQ ID NO:35 corresponds to GenBank accession number AF245704, which is a nucleotide
 10 sequence of human TLR9 cDNA. SEQ ID NO:36 is a nucleotide sequence of human cDNA encoding amino acids 1-820 of SEQ ID NO:33.

SEQ ID NO:29 (Murine TLR9)

MVLRRRTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAASCSNITRLSLISNRI
 15 HHLHNSDFVHLSNLRQLNLKWNCPPTGLSPLHFSCMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNLSL
 SHTNIVLDANSLAGLYSLRVLFMDGNCYYKNPCTGAVKVTPGALLGLSNLTHLSLKYNNTKVPRQLPPSLEYL
 LVSYNLIVKLGPEDLANLTSLRVLDVGGNCRRCDHAPNPCIECGQKSLHLHPETFHHLSHLEGLVLKDDSSLHTLN
 SSWFQGLVNLSVLDLSENFLYESINHNTAFQNLTRLRKLNLNLSFNRYKKVSFARLHLASSFKNLVSLQELNMNGIF
 20 FRSLNKYTLRWLADLPKLHTLHLQMNFINQAQLSIFGTFRALRFVDLSDNRIISGPSTLSEATPEEADDAEQEELL
 SADPHAPLPSTPASKNFMDRCKNFKFTMDLSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ
 VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFSMKGIGHNFSFVAHLSMLHSLSLAHNDIHRVSSHLSNS
 VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKLDLSQNNLHILRPQNLNLPKSLKLLSLRDNYLSFFNWTSL
 25 FLNLEVLDDLGNQKALTNGTLPNGTLLQKLDVSSNSIVSVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV
 MNLTVLVDVRSNPLHCACGAADFVLDLLEVTQKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFLSLL
 AVAVGMVVPILHHLGWDVWYCFHLCLAWPLLLARSRRSAQALPYDAFVVFDAQSAVADWVYNELRVRLERRG
 RRALRLCLEDRDWLPQGTLFENLWASIYGRKTLFVLAHTDRVSGLLRTSFLLAQQRLLDRKDVVVLVILRPDA
 HRSRYVRLRQRLCRQSVLFWPQQPNGQGFWAQLSTALTRDNRHFYNQNFRCGPAT

SEQ ID NO:30 (Murine TLR9)

MVLRRRTLHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAAASCSNITRLSLISNRI
 30 HHLHNSDFVHLSNLRQLNLKWNCPPTGLSPLHFSCMTIEPRTFLAMRTLEELNLSYNGITTVPRLPSSLVNLSL
 SHTNIVLDANSLAGLYSLRVLFMDGNCYYKNPCTGAVKVTPGALLGLSNLTHLSLKYNNTKVPRQLPPSLEYL
 LVSYNLIVKLGPEDLANLTSLRVLDVGGNCRRCDHAPNPCIECGQKSLHLHPETFHHLSHLEGLVLKDDSSLHTLN
 35 SSWFQGLVNLSVLDLSENFLYESINHNTAFQNLTRLRKLNLNLSFNRYKKVSFARLHLASSFKNLVSLQELNMNGIF
 FRSLNKYTLRWLADLPKLHTLHLQMNFINQAQLSIFGTFRALRFVDLSDNRIISGPSTLSEATPEEADDAEQEELL
 SADPHAPLPSTPASKNFMDRCKNFKFTMDLSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQ
 VLDLSHNKLDLYHWKSFSELPQLQALDLSYNSQPFSMKGIGHNFSFVAHLSMLHSLSLAHNDIHRVSSHLSNS
 VRFLDFSGNGMGRMWDEGGLYLHFFQGLSGLLKLDLSQNNLHILRPQNLNLPKSLKLLSLRDNYLSFFNWTSL
 40 FLNLEVLDDLGNQKALTNGTLPNGTLLQKLDVSSNSIVSVPAFFALAVELKEVNLSHNILKTVDRSWFGPIV
 MNLTVLVDVRSNPLHCACGAADFVLDLLEVTQKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFG

SEQ ID NO:31 (Murine TLR9)

tgtcagagggagcctcgaggagaatcctccatctcccaacatggttctccgctcgaaggactctgcaccccttgtcc
 ctccctgggtacaggctgcagtgctggctgagactctggccctgggtaccctgcctgccttcctaccctgtgagctg

- 25 -

aagcctcatggcctggtggactgcaattggctgttcctgaagtctgtaccccggtttctctgcggcagcatcctgc
tccaacatcaccgcctctccttgatctccaaccgtatccaccacctgcacaactccgacttcgtccacctgtcc
aacctgcggcagctgaacctcaagtggaaactgtccaccactggccttagccccctgcacttctcttgccacatg
accattgagcccagaaccttctctggctatgagctacactggaggagctgaacctgagctataatgggtatcaccact
5 gtgccccgactgccagctccctgggtgaatctgagcctgagccacaccaacatcctgggttctagatgctaacagc
ctcgccggtctatacagcctgcgcgttctcttcatggacgggaactgctactacaagaacccccgcacaggagcg
gtgaagggtgaccccaggcgccctcctgggcctgagcaatctcaccatctgtctctgaagtataacaacctcaca
aagggtgccccgcaactgccccccagcctggagtagctcctgggtgtcctataacctcattgtcaagctggggcct
gaagacctggccaacttgacctcccttcgagtacttgatgtgggtgggaattgcgctcgctgcgacctgcccc
10 aatccctgtatagaatgtggccaaaagtcctccacctgcacctgagacctccatcacctgagccatctggaa
ggcctgggtgctgaaggagacgtctctccatacactgaactcttctgggttccaaggctggtcaacctctcggtg
ctggacctaaagcgagaaacttctctatgaaagcatcaaccaccaatgccttccagaacctaacccgctgcgc
aagctcaacctgtccttcaattaccgcaagaaggatccttctggcctccacctggcaagttccttcaagaac
ctgggtgctcactgcaggagctgaacatgaacggcatcttcttccgctcgctcaacaagtacacgctcagatggctg
15 gccgatctgccccaaactccacactctgcatcttcaaatgaacttcatcaaccaggcacagctcagatcttgggt
accttccgagcccttcgcttctgtggacttgtcagacaatcgcatcagtgggccttcaacgctgtcagaagccacc
cctgaagaggcagatgatgcagagcaggaggagctgttctgctgaggatcctcaccagctccactgagcaccct
gcttctaagaacttcatggacaggtgtaagaacttcaagttcaccatggacctgtctcggaacaacctgggtgact
atcaagccagagatgttctgcaatctctcagcctccagtgctttagcctgagccacaactccattgcacaggct
20 gtcaatgggtctcagttcctgcccgtgactaatctgcaggtgctggacctgtcccataacaaactggacttgtac
cactggaaatcggtcagtgagctaccacagttgcaggccctggacctgagctacaacagccagccctttagcatg
aagggtataggccacaattttagtcttctggtggccatctgtccatgctacacagccttagcctggcacacaatgac
attcatacccggtgtgtcctcacatctcaacagcaactcagtgaggttctttagcttcagcggcaacgggtatgggc
cgcatgtgggatgaggggggcttctctccatttcttccaaggcctgagtggtgctgaagctggacctgtct
25 caaaataacctgcatactcctccggccccagaaccttgacaacctccccaaagagcctgaagctgctgagcctccga
gacaactacctatcttctttaaactggaccagtctgtccttccctgccccaaactggaagtccttagacctggcaggc
aaccagctaaaggccctgaccaatggcaccctgcctaattggcaccctcctccagaaactggatgtcagcagcaac
agtatcgtctctgtggtcccagccttcttctgctctggcggtcgagctgaaagaggtcaacctcagccacaacatt
ctcaagacgggtggatcgctcctgggttgggcccattgtgatgaacctgacagttctagacgtgagaagcaacct
30 ctgcaactgtgctgtggggcagccttcgtagacttactgttggagggtgcagaccaaggtgcctggcctggcta
gggtgtgaagtgtggcagccccggcagctgcaggccgtagcatcttgcacaggacctggcgtgtgcttggat
gaggtcctctcttgggactgcttggccttctcactcttggctgtggcctggtggtggtgcttactgac
catctctgcggtgggagctgtggtactgttcttcatctgtgcttggcatggctaccttggctggcccgagccga
cgcagcggcccaagctctccctatgtatgccttctggtgttcgataaggcacagagcgcagttgcggactgggtg
35 tataacgagctgcgggtgcggctggaggagcggcgcggtcgccagccctacgcttgtgtctggaggaccgagat
tggtgctgctggccagacgctcttcgagaacctctgggcttccatctatggggagcgcgaagactctattgtgctg
gcccacacggaccgcgtcagtggtcctcctgctgacccagcttctgctggctcagcagcgcctgttgggaagaccgc
aaggacgtgggtgtgtggtgatcctgcgtccggatgccaccgctcccgtatgtgagactgcgccagcgtctc
tgccgccagagtggtgctcttctggccccagcagcccaacgggcaggggggtcttggggccagctgagtagcagcc
40 ctgactagggacaacggccacttctataaccagaactctgcgggggacctacagcagaatagctcagagcaaca
gctggaaacagctgcactcttcatgcctgggttcccaggtgtgctgctgctgc

SEQ ID NO:31 (Murine TLR9)

atgggttctccgctgaaggactctgcaccccttgtccctcctggtagagctgcagtgctggctgagactctggcc
45 ctgggtaccctgcctgccttccctaccctgtgagctgaagcctcatggcctgggtggactgcaattggctgttccgtg
aagtctgtaccccggtttctctgcggcagcatcctgctccaacatcaccgcctctccttgatctccaaccgtatc
caccacctgcacaactccgacttcgtccacctgtccaacctgcggcagctgaacctcaagtggaaactgtccacc
actggccttagccccctgcacttctcttggccatgaccttgagccagaaccttctggctatgcgtacactg
gaggagctgaacctgagctataatgggtatcaccactgtgccccgactgccagctccctgggtgaatctgagcctg
50 agccacaccaacatcctgggttctagatgctaacagcctcgccggcctatacagcctgcgcgttctcttcatggac
gggaactgctactacaagaacccccgcacaggagcgggtgaagggtgaccccaggcgccctcctgggcctgagcaat
ctcaccatctgtctctgaagtataacaacctcacaagggtgccccgccaactgccccccagcctggagtagctc
ctgggtgtcctataacctcattgtcaagctggggcctgaagacctggccaatctgacctcccttcgagtacttgat
gtgggtgggaattgcgctcgctgcgacctgcccccaatccctgtatagaatgtggccaaaagtcctccacctg
55 caccctgagaccttccatcacctgagccatctggaaggcctgggtgctgaaggacagctctctccatacactgaac
tcttctgggttccaaggctggtgcaacctctcggtgctggacctaaagcgagaacttctctatgaaagcatcaac
cacaccaatgccttccagaacctaacccgctgcgaagctcaacctgtccttcaattaccgcaagaaggatcc

- 26 -

tttgcccgcctccacctggcaagttccttcaagaacctgggtgtcactgcaggagctgaacatgaacggcatcttc
 ttccgctcgctcaacaagtaacagctcagatggctggccgatctgcccactccacactctgcatcttcaaag
 aacttcatcaaccaggacagctcagcatcttgggtaccttccgagcccttcgcttgggtgactgtcagacaat
 5 cgcacagtggtggccttcaacgctgtcagaagccaccctgaagaggcagatgatgcagagcaggaggagctgttg
 ttgoggatcctcaccagctccactgagcaccctgcttctaagaacttcatggacaggtgtaagaacttcaag
 ttaccatggacctgtctcggaacaacctgggtgactatcaagccagagatgtttgtcaatctctcacgcctccag
 tgtcttagcctgagccacaactccattgcacaggctgtcaatggctctcagttcctgcccgtgactaatctgcag
 gtgctggacctgtcccataacaaactggactgtaccactggaaatcggtcagtgagctaccacagttgcaggcc
 ctggacctgagctacaacagccagccctttagcatgaagggtataggccacaatttcagtttgggtggccatctg
 10 tccatgctacacagccttagcctggcacacaatgacattcataccgtgtgtcctcacatctcaacagcaactca
 gtgaggtttcttgacttcagcggcaacggtatggggcgcagtggtggatgaggggggctttatctccatttcttc
 caaggcctgagtggtcctgtgaagctggacctgtctcaaaataacctgcatatcctccggccccagaaccttgac
 aacctccccaaagagcctgaagctgctgagcctccgagacaactacctatctttctttaactggaccagtctgtcc
 ttctgccccaaacctggaagtcttagacctggcaggcaaccagctaaaggccctgaccaatggcaccctgccta
 15 ggcaccctcctccagaaactggatgtcagcagcaacagtatcgtctctgtggtcccagccttcttcgctctggcg
 gtcgagctgaaagaggtcaacctcagccacaacatttcaagacgggtggatcgctcctgggttgggcccattgtg
 atgaacctgacagttcttagacgtgagaagcaacctctgcactgtgcctgtggggcagccttcgtagacttactg
 ttggaggtgcagaccaaggtgcctggcctggctaataaggtgtgaagtgtggcagccccggccagctgcaggggcgt
 agcatcttcgcacaggacctgcggctgtgcctggatgaggtcctctcttgggactgctttggc
 20

SEQ ID NO:33 (Human TLR9)

MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWFLKSVPHFSMAAPRGNVTSLSLSSNRI
 HHLHDSDFAHLPRLRLNLKWNCPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSL
 SHTNILMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNTTVPRNLPSSLEYL
 25 LLSYNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPMCPCPRHFPQLHPDTFSHLRLEGLVLKDSLSWLN
 ASWFRGLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLNFYQKRVSFAHLSLAPSFGLVALKELDMHGIF
 FRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGADGGEKVLQ
 GD LAPAPVDTPSSEDFRPNCTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV
 LDLSRNKLDLYHEHSFTELPRLEALDLSYNSQPFMGQGVGHNFVFAHLRTLRLSLAHNNIHSQVSQQLCSTSL
 30 RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNLRLHTLLPQTLRLNLPKSLQVLRRLDNYLAFFKWWSLHF
 LPKLEVLDLAGNRLKALTNGSLPAGTRLRLRLDVSCNSISFVAPGFFSKAKELRELNLNLSANALKTVDHWSFGPLAS
 ALQILDV SANPLHCACGA AFMDFLLEVQA AVPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALS WDCFALSLLA
 VALGLGVPM LHHLCGWDLYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVDKTQSAVADWVYNELRGQLEECRG
 RWALRLCLEERD WLP GKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLL EDRKD VVVLVILSPDG
 35 RRSRYVRLRQRLCRQS VLLWPHQPSGQRSFQAQLGMALTRDNH HFYNRNFCQGP TAE

SEQ ID NO:34 (Human TLR9)

MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWFLKSVPHFSMAAPRGNVTSLSLSSNRI
 HHLHDSDFAHLPRLRLNLKWNCPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSL
 40 SHTNILMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNTTVPRNLPSSLEYL
 LLSYNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPMCPCPRHFPQLHPDTFSHLRLEGLVLKDSLSWLN
 ASWFRGLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLNFYQKRVSFAHLSLAPSFGLVALKELDMHGIF
 FRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGADGGEKVLQ
 GD LAPAPVDTPSSEDFRPNCTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQV
 45 LDLSRNKLDLYHEHSFTELPRLEALDLSYNSQPFMGQGVGHNFVFAHLRTLRLSLAHNNIHSQVSQQLCSTSL
 RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNLRLHTLLPQTLRLNLPKSLQVLRRLDNYLAFFKWWSLHF
 LPKLEVLDLAGNRLKALTNGSLPAGTRLRLRLDVSCNSISFVAPGFFSKAKELRELNLNLSANALKTVDHWSFGPLAS
 ALQILDV SANPLHCACGA AFMDFLLEVQA AVPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALS WDCFA

50 SEQ ID NO:35 (Human TLR9)

aggcgtggtataaaaaatcttacttctctattctctctgagccgctgctgcccctgtgggaaggacacctcgagtgtga
 agcatccttccctgtagctgctgtccagtctgcccgcagaccctctggagaagccctgccccccagcatgggt
 ttctgcccgcagcgcctgcacccgctgtctctctggtgcaggccatcatgctggccatgacctggccctgggt

- 27 -

accttgccctgccttccctaccctgtgagctccagccccacggcctggtgaactgcaactggctgttccctgaagtct
gtgccccactttctccatggcagcaccctggtgcaatgtcaccagcctttccctgtcctccaaccgcacccaccac
ctccatgattctgactttgcccacctgcccagcctgcgccatctcaacctcaagtggaaactgcccgcgggttggc
ctcagccccatgcacttcccctgccacatgaccatcgagcccagcaccttcttggctgtgcccacccctggaagag
5 ctaaacctgagctacaacaacatcatgactgtgcctgcgctgcccaaatccctcatatccctgtccctcagccat
accaacatccctgatgctagactctgccagcctcgccggcctgcatgcctgcgcttccctattcatggacgggaac
tggtattacaagaacccctgcaggcaggcactggaggtggccccgggtgccctcccttggcctgggcaacctcacc
cacctgtcactcaagtacaacaacctcactgtggtgccccgcaacctgccttccagcctggagtatctgctgttg
tccataaacccgcacgtcaaaactggcgccctgaggacctggccaatctgaccgcccctgcgtgtgctcgatgtgggc
10 ggaaattgcccgcgctgcgaccacgctcccaacccctgcatggagtgcctcgtcacttccccagctacatccc
gataccttcagccacctgagccgtcttgaaggcctggtgttgaaggacagttctctctccttggctgaatgccagt
tgggttccgtgggctgggaaacctccgagtgtgacctgagtgagaacttccctctacaaatgcatcactaaaacc
aaggccttccagggcctaacacagctgcgcaagcttaacctgtccttcaattacaaaagaggggtgtcctttgcc
cacctgtctctggcccccttccctcgggagcctggtcgccctgaaggagctggacatgcacggcatcttcttcgc
15 tcaactcgatgagaccacgctccggccactggccgcctgcccattgctccagactctgcgtctgcagatgaacttc
atcaacaggcccgagctcggcatcttcagggccttccctggcctgcgctacgtggacctgtcggacaacccgcatc
agcggagcttcggagctgacagccaccatgggggaggcagatggaggggagaaggctctggctgcagcctggggac
cttgctccggccccagtggaactcctcagctctgaagacttcaggcccaactgcagcaccctcaacttcaccttg
gatctgtcacggaacaacctggtgacctgcagccggagatgtttgccagctctcgcacctgcagtgcctgcgc
20 ctgagccacaactgcatctcgcaggcagtcattggctcccagttcctgcccgtgaccggctctgcaggtgctagac
ctgtcccgaataagctggacctctaccacgagcactcattcacggagctaccgcgactggaggccctggacctc
agctacaacagccagccctttggcatgcaggcgctggggccacaacttcagcttcgtggctcacctgcgcacctg
cgccacctcagcctggcccacaacaacatccacagccaagtgtccagcagctctgcagtacgtcgctgcggggcc
ctggacttcagcggcaatgcactgggcatatgtggggcggaggagacctctatctgcacttcttccaaggcctg
25 agcgggttgatctggctggacttgtcccagaaccgcctgcacacctcctgccccaaacctgcgcaacctcccc
aagagcctacaggtgctgcgtctccgtgacaattacctggccttctttaagtgggtggagcctccacttccctgcc
aaactggaagtcctcgacctggcaggaaaccggctgaaggccctgaccaatggcagcctgcctgctggcaccg
ctccggaggctggatgtcagctgcaacagcatcagcttccgtggcccccggttcttttccaaggccaaggagctg
cgagagctcaaccttagcgccaacgcctcaagacagtggaccactcctgggttggggccctggcgagtgcctg
30 caaatactagatgtaagcgccaacctctgcactgcgcctgtggggcgccctttatggacttccctgctggagggtg
caggctgcccgtgcccggctctgccagccgggtgaagtgtggcagtcggggccagctccagggcctcagcatctt
gcacaggacctgcgcctctgctggatgaggccctctcctgggactgtttcgccctctcgtgctggctgtggct
ctgggcctgggtgtgcccattgctgcatcacctctgtggctgggacctctggtactgcttccacctgtgcctggcc
tggcttccctggcgggggcggaagtggcgagatgaggatgcctgcccctacgatgccttcgtggtcttcgac
35 aaaacgcagagcgcagtggcagactgggtgtacaacgagcttcgggggcagctggaggagtgcctgaggcgtgg
gcactccgctgtgctggaggaaacgcgactggctggcggcaaacctcttgagaacctgtgggacctcggtc
tatggcagccgcaagcgtgtttgtgctggccacacggaccgggtcagtggtctcttgcgcgccagcttccctg
ctggcccagcagcgctgctggaggaccgcaaggacgtcgtggtgctggtgatcctgagccctgacggccgcccgc
tcccgtacgtgcggctgcgccagcgctctgcccagagtgctcctcctctggccccaccagccagtggtcag
40 cgcagcttctggggccagctgggcatggccctgaccagggaacaaccaccttctataaccggaacttctgccag
ggaccacagggccgaatagccgtgagccggaatcctgcaggtgccacctccacactcacctcacctctgcctgcc
tggctgaccttccctgctgcctccctcaccacacactgacacagagca

SEQ ID NO:36 (Human TLR9)

45 atgggtttctgccgagcgccctgcaccgcgtgtctctcctgggtgagggccatcatgctggccatgacctggcc
ctgggtaccttgctgccttccctaccctgtgagctccagccccacggcctggtgaactgcaactggctgttccctg
aagtctgtgcccacttctccatggcagcaccctggtgcaatgtcaccagcctttccctgtcctccaaccgcac
caccacctccatgattctgactttgcccacctgcccagcctgcgccatctcaacctcaagtggaaactgcccgcg
gttggcctcagccccatgcacttcccctgccacatgaccatcgagcccagcaccttcttggctgtgcccacctg
50 gaagagctaaacctgagctacaacaacatcatgactgtgcctgcgctgccccaaatccctcatatccctgtccctc
agccataccaacatccctgatgctagactctgccagcctcgccggcctgcatgcctgcgcttccctattcatggac
ggcaactgttattacaagaacccctgcaggcaggcactggaggtggccccgggtgccctccttggcctggggaac
ctcaccacactgtcactcaagtacaacaacctcactgtggtgccccgcaacctgccttccagcctggagtatctg
ctggtgtcctacaaccgcacgtcaaaactggcgccctgaggacctggccaatctgaccgcccctgcgtgtgctcgat
55 gtggggcggaattgcccgcgctgcgaccacgctcccaacccctgcatggagtgcctcgtcacttccccagcta
catcccgataccttcagccacctgagccgtcttgaaggcctggtgttgaaggacagttctctctcctggctgaat
gccagttgggtccgtgggctgggaaacctccgagtgtggaacctgagtgagaacttccctctacaaatgcatcact

- 28 -

aaaaccaaggccttccagggcctaacacagctgcgcaagcttaacctgtccttcaattaccaaagaggggtgtcc
 tttgcccacctgtctctggtggcccttcccttcgggagcctggctgcacctgaaggagctggacatgcacggcatcttc
 tccgctcactcgtatgagaccacgctccggccactggcccgctgcccatgctccagactctgctgctgcagatg
 aacttcatcaaccaggcccagctcggcatcttcagggccttccctggcctgcgctacgtggacctgtcggacaac
 5 cgcacacagcggagcttcggagctgacagccaccatgggggagggcagatggaggggagaaggtctggctgcagcct
 ggggaccttgctccggccccagtggaactcccagctctgaagacttcaggcccaactgcagcaccctcaacttc
 accttggatctgtcacggaacaacctgggtgacctgcagccggagatggttggccagctctcgcacctgcagtg
 ctgacctgagccacaactgcatctcgcaggcagtcgaatggctcccagttcctgcccgtgaccggctgtgcaggtg
 10 ctagacctgtcccgcaataagctggacctctaccacgagcactcattcacggagctaccgcgactggaggccctg
 gacctcagctacaacagccagcccttggcatgcagggcgtggggccacaacttcagcttcgtggctcacctgcgc
 accctgcgccacctcagcctggcccaacaacatccacagccaagtgtcccagcagctctgcagtacgtcgtg
 cgggacctggacttcagcggcaatgcactgggcatatgtgggcccagggagacctctatctgcacttcttccaa
 ggctgagcgggttgatctggctggacttgctccagaaccgcctgcacacctcctgccccaaacctgcgcaac
 ctcccaagagcctacaggtgctgctcctcgtgacaattacctggccttctttaagtggaggcctccacttc
 15 ctgccccaaactggaagtcctcgcacctggcaggaaccggctgaaggccctgaccaatggcagcctgcctgtggc
 acccggtccggaggctggatgtcagctgcaacagcatcagcttcgtggcccccggttcttttccaaggccaag
 gagctgcgagagctcaaccttagcgccaacgcctcaagacagtggaaccactcctgggttggggccctggcgagt
 gccctgcaataactagatgtaagcgccaacctctgcactgcgcctgtggggcgccctttaggacttctgctg
 gaggtgcaggctgccgtgccggctgcccagccgggtgaagtgtggcagtcggggccagctccagggcctcagc
 20 atctttgcacaggacctgcgcctctgcctggatgaggccctctcctgggactgtttcgcc

In addition to the foregoing native rat, porcine, bovine, equine, and ovine TLR9
 polypeptides and nucleic acid molecules encoding them, chimeric TLR9 polypeptides and
 nucleic acid molecules encoding them are provided by the invention. The chimeric
 25 polypeptides include at least one amino acid substitution based on a comparison of
 conserved and non-conserved amino acids among at least two of rat, murine, porcine, bovine,
 equine, ovine, canine, feline, and human TLR9. The information contained in a multiple
 sequence alignment of these various TLR9 polypeptide sequences, provided for example in
 Figure 1, can be used to identify and select individual amino acid positions and even
 30 individual amino acids to substitute in designing a chimeric TLR9. The substitution or
 substitutions can be effected using methods known to those of ordinary skill in molecular
 biology. Nucleic acids encoding the native or chimeric polypeptides of the invention can be
 inserted into an expression vector and used to express TLR9 polypeptide.

A conservative amino acid substitution shall refer to a substitution of a first amino
 35 acid for a second amino acid, wherein side chains of the first amino acid and the second
 amino acid share similar features in terms of hydrophobicity, size, aromaticity, or tendency to
 alter conformation. For example, conservative amino acid substitutions generally may be
 made between members within each of the following groups: hydrophobic (A, I, L, M, V),
 neutral (C, S, T), acidic (D, E), basic (H, K, N, Q, R), and aromatic (F, W, Y). A non-
 40 conservative amino acid substitution refers to any other amino acid substitution.

- 29 -

An expression vector for TLR9 will include at least a nucleotide sequence coding for a TLR9, or a fragment thereof coding for a functional TLR9 polypeptide, operably linked to a gene expression sequence which can direct the expression of the TLR9 nucleic acid within a eukaryotic or prokaryotic cell. A "gene expression sequence" is any regulatory nucleotide
5 sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the nucleic acid to which it is operably linked.

With respect to TLR9 nucleic acid, the "gene expression sequence" is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the TLR9 nucleic acid to which it is
10 operably linked. The gene expression sequence may, for example, be a mammalian or viral promoter, such as a constitutive or inducible promoter. Constitutive mammalian promoters include, but are not limited to, the promoters for the following genes: hypoxanthine phosphoribosyl transferase (HPRT), adenosine deaminase, pyruvate kinase, β -actin promoter, and other constitutive promoters. Exemplary viral promoters which function constitutively in
15 eukaryotic cells include, for example, promoters from the simian virus (e.g., SV40), papillomavirus, adenovirus, human immunodeficiency virus (HIV), Rous sarcoma virus (RSV), cytomegalovirus (CMV), the long terminal repeats (LTR) of Moloney murine leukemia virus and other retroviruses, and the thymidine kinase (TK) promoter of herpes simplex virus. Other constitutive promoters are known to those of ordinary skill in the art.
20 The promoters useful as gene expression sequences of the invention also include inducible promoters. Inducible promoters are expressed in the presence of an inducing agent. For example, the metallothionein (MT) promoter is induced to promote transcription and translation in the presence of certain metal ions. Other inducible promoters are known to those of ordinary skill in the art.

25 In general, the gene expression sequence shall include, as necessary, 5' non-transcribing and 5' non-translating sequences involved with the initiation of transcription and translation, respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribing sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined nucleic acid
30 coding sequence for a TLR9 polypeptide. The gene expression sequences optionally include enhancer sequences or upstream activator sequences as desired.

- 30 -

Generally a nucleic acid coding sequence and a gene expression sequence are said to be “operably linked” when they are covalently linked in such a way as to place the transcription and/or translation of the nucleic acid coding sequence under the influence or control of the gene expression sequence. Thus the TLR9 nucleic acid coding sequence and the gene expression sequence are said to be “operably linked” when they are covalently linked in such a way as to place the transcription and/or translation of the TLR9 nucleic acid coding sequence under the influence or control of the gene expression sequence. If it is desired that the TLR9 sequence be translated into a functional protein, two DNA sequences are said to be operably linked if induction of a promoter in the 5' gene expression sequence results in the transcription of the TLR9 sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the TLR9 sequence, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a gene expression sequence would be operably linked to a TLR9 nucleic acid sequence if the gene expression sequence were capable of effecting transcription of that TLR9 nucleic acid sequence such that the resulting transcript might be translated into the desired TLR9 protein or polypeptide.

A “TLR9 ligand” as used herein refers to a molecule that specifically binds a TLR9 polypeptide. In one embodiment the TLR9 ligand specifically binds a TLR9 polypeptide corresponding to at least a ligand-binding portion of the extracellular domain of TLR9. In most instances a TLR9 ligand will also induce TLR9 signaling when contacted with TLR9 under suitable conditions. TLR9 signaling refers to TLR/IL-1R signal transduction mediated through the TLR9, as described in further detail elsewhere herein. As mentioned above, CpG nucleic acids have been reported to be TLR9 ligands, but TLR9 ligands may include other entities as well, including, for example, small molecules. As also previously mentioned, there appears to be a species-specific preference for at least certain TLR9s and certain CpG motifs. As used herein, a species-preferred CpG DNA refers to a particular CpG DNA that is optimized for signal induction by a TLR9 of a particular species. A CpG DNA that is optimized for signal induction by a TLR9 of a particular species refers to a CpG DNA having a sequence that preferentially binds to and/or induces signaling by TLR9 of that species. For example, a human-preferred CpG DNA shall refer to a CpG DNA that optimally stimulates human TLR9 to signal through its TIR domain. Likewise, a murine-preferred CpG DNA

- 31 -

shall refer to a CpG DNA that optimally stimulates murine TLR9 to signal through its TIR domain. Examples of human-preferred and murine-preferred CpG DNA are ODN 2006 (SEQ ID NO:58) and 1668 (SEQ ID NO:60), respectively.

The binding and species specificity of TLR9s are believed to be influenced by key amino acids present in the extracellular domain of TLR9. Key amino acids in a TLR9 as used herein refer to those amino acids which contribute significantly to ligand binding and ligand specificity of a particular TLR9 polypeptide.

A "CpG nucleic acid" or a "CpG immunostimulatory nucleic acid" as used herein is a nucleic acid containing at least one unmethylated CpG dinucleotide (cytosine-guanine dinucleotide sequence, i.e., "CpG DNA" or DNA containing a 5' cytosine followed by 3' guanine and linked by a phosphate bond) which activates a component of the immune system. The entire CpG nucleic acid can be unmethylated or portions may be unmethylated but at least the C of the 5' CG 3' must be unmethylated.

In one embodiment a CpG nucleic acid is represented by at least the formula:



wherein X_1 and X_2 are nucleotides, N is any nucleotide, and N_1 and N_2 are nucleic acid sequences composed of from about 0-25 N's each. In some embodiments X_1 is adenine, guanine, or thymine and/or X_2 is cytosine, adenine, or thymine. In other embodiments X_1 is cytosine and/or X_2 is guanine.

Nucleic acids having modified backbones, such as phosphorothioate backbones, also fall within the class of immunostimulatory nucleic acids. U.S. Pat. Nos. 5,723,335 and 5,663,153 issued to Hutcherson, et al. and related PCT publication WO95/26204 describe immune stimulation using phosphorothioate oligonucleotide analogues. These patents describe the ability of the phosphorothioate backbone to stimulate an immune response in a non-sequence specific manner.

An immunostimulatory nucleic acid molecule, including for example a CpG DNA, may be double-stranded or single-stranded. Generally, double-stranded molecules may be more stable *in vivo*, while single-stranded molecules may have increased activity. The terms "nucleic acid" and "oligonucleotide" refer to multiple nucleotides (i.e., molecules comprising a sugar (e.g., ribose or deoxyribose) linked to a phosphate group and to an exchangeable organic base, which is either a substituted pyrimidine (e.g., cytosine (C), thymine (T) or uracil (U)) or a substituted purine (e.g., adenine (A) or guanine (G)) or a modified base. As

- 32 -

used herein, the terms "nucleic acid" and "oligonucleotide" refer to oligoribonucleotides as well as oligodeoxyribonucleotides. The terms shall also include polynucleosides (i.e., a polynucleotide minus the phosphate) and any other organic base-containing polymer. The terms "nucleic acid" and "oligonucleotide" also encompass nucleic acids or oligonucleotides with a covalently modified base and/or sugar. For example, they include nucleic acids having backbone sugars which are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 2' position and other than a phosphate group at the 5' position. Thus modified nucleic acids may include a 2'-O-alkylated ribose group. In addition, modified nucleic acids may include sugars such as arabinose instead of ribose. Thus the nucleic acids may be heterogeneous in backbone composition thereby containing any possible combination of polymer units linked together such as peptide-nucleic acids (which have amino acid backbone with nucleic acid bases). In some embodiments the nucleic acids are homogeneous in backbone composition.

The substituted purines and pyrimidines of the immunostimulatory nucleic acids include standard purines and pyrimidines such as cytosine as well as base analogs such as C-5 propyne substituted bases. Wagner RW et al. (1996) *Nat Biotechnol* 14:840-4. Purines and pyrimidines include but are not limited to adenine, cytosine, guanine, thymine, 5-methylcytosine, 2-aminopurine, 2-amino-6-chloropurine, 2,6-diaminopurine, hypoxanthine, and other naturally and non-naturally occurring nucleobases, substituted and unsubstituted aromatic moieties.

The immunostimulatory nucleic acid is a linked polymer of bases or nucleotides. As used herein with respect to linked units of a nucleic acid, "linked" or "linkage" means two entities are bound to one another by any physicochemical means. Any linkage known to those of ordinary skill in the art, covalent or non-covalent, is embraced. Such linkages are well known to those of ordinary skill in the art. Natural linkages, which are those ordinarily found in nature connecting the individual units of a nucleic acid, are most common. The individual units of a nucleic acid may be linked, however, by synthetic or modified linkages.

Whenever a nucleic acid is represented by a sequence of letters it will be understood that the nucleotides are in 5' to 3' (or equivalent) order from left to right and that "A" denotes adenine, "C" denotes cytosine, "G" denotes guanine, "T" denotes thymidine, and "U" denotes uracil unless otherwise noted.

Immunostimulatory nucleic acid molecules useful according to the invention can be obtained from natural nucleic acid sources (e.g., genomic nuclear or mitochondrial DNA or cDNA), or are synthetic (e.g., produced by oligonucleotide synthesis). Nucleic acids isolated from existing nucleic acid sources are referred to herein as native, natural, or isolated nucleic acids. The nucleic acids useful according to the invention may be isolated from any source, including eukaryotic sources, prokaryotic sources, nuclear DNA, mitochondrial DNA, etc. Thus, the term nucleic acid encompasses both synthetic and isolated nucleic acids.

The immunostimulatory nucleic acids can be produced on a large scale in plasmids, (see *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989) and separated into smaller pieces or administered whole. After being administered to a subject the plasmid can be degraded into oligonucleotides. One skilled in the art can purify viral, bacterial, eukaryotic, etc. nucleic acids using standard techniques, such as those employing restriction enzymes, exonucleases or endonucleases.

For use in the instant invention, the immunostimulatory nucleic acids can be synthesized *de novo* using any of a number of procedures well known in the art. For example, the β -cyanoethyl phosphoramidite method (Beaucage SL and Caruthers MH, *Tetrahedron Let* 22:1859 (1981)); nucleoside H-phosphonate method (Garegg et al., *Tetrahedron Let* 27:4051-4054 (1986); Froehler et al., *Nucl Acid Res* 14:5399-5407 (1986); Garegg et al., *Tetrahedron Let* 27:4055-4058 (1986); Gaffney et al., *Tetrahedron Let* 29:2619-2622 (1988)). These chemistries can be performed by a variety of automated oligonucleotide synthesizers available in the market.

The immunostimulatory nucleic acid may be any size of at least 6 nucleotides but in some embodiments are in the range of between 6 and 100 or in some embodiments between 8 and 35 nucleotides in size. Immunostimulatory nucleic acids can be produced on a large scale in plasmids. These may be administered in plasmid form or alternatively they can be degraded into oligonucleotides before administration.

A "stabilized immunostimulatory nucleic acid" shall mean a nucleic acid molecule that is relatively resistant to *in vivo* degradation (e.g., via an exo- or endo-nuclease).

Stabilization can be a function of length or secondary structure. Nucleic acids that are tens to hundreds of kbs long are relatively resistant to *in vivo* degradation. For shorter nucleic acids, secondary structure can stabilize and increase their effect. For example, if the 3' end of an

- 34 -

oligonucleotide has self-complementarity to an upstream region, so that it can fold back and form a sort of stem loop structure, then the oligonucleotide becomes stabilized and therefore exhibits more activity.

Some stabilized immunostimulatory nucleic acids have a modified backbone. It has been demonstrated that modification of the oligonucleotide backbone provides enhanced activity of the immunostimulatory nucleic acids when administered *in vivo*. Nucleic acids, including at least two phosphorothioate linkages at the 5' end of the oligonucleotide and multiple phosphorothioate linkages at the 3' end, preferably 5, may provide maximal activity and protect the oligonucleotide from degradation by intracellular exo- and endo-nucleases.

Other modified oligonucleotides include phosphodiester modified oligonucleotide, combinations of phosphodiester and phosphorothioate oligonucleotide, methylphosphonate, methylphosphorothioate, phosphorodithioate, and combinations thereof. Each of these combinations and their particular effects on immune cells is discussed in more detail in U.S. Pat. Nos. 6,194,388 and 6,207,646, the entire contents of which are incorporated herein by reference. It is believed that these modified oligonucleotides may show more stimulatory activity due to enhanced nuclease resistance, increased cellular uptake, increased protein binding, and/or altered intracellular localization. Both phosphorothioate and phosphodiester nucleic acids are active in immune cells.

Other stabilized immunostimulatory nucleic acids include: nonionic DNA analogs, such as alkyl- and aryl-phosphates (in which the charged phosphonate oxygen is replaced by an alkyl or aryl group), phosphodiester and alkylphosphotriesters, in which the charged oxygen moiety is alkylated. Oligonucleotides which contain diol, such as tetraethyleneglycol or hexaethyleneglycol, at either or both termini have also been shown to be substantially resistant to nuclease degradation.

Phosphorothioate nucleic acid molecules may be synthesized using automated techniques employing either phosphoramidate or H-phosphonate chemistries. Aryl- and alkyl-phosphonates can be made, e.g., as described in U.S. Pat. No. 4,469,863; and alkylphosphotriesters (in which the charged oxygen moiety is alkylated as described in U.S. Pat. No. 5,023,243 and European Patent No. 092,574) can be prepared by automated solid phase synthesis using commercially available reagents. Methods for making other DNA backbone modifications and substitutions have been described. Uhlmann E and Peyman A (1990) *Chem Rev* 90:544; Goodchild J (1990) *Bioconjugate Chem* 1:165.

- 35 -

Other sources of immunostimulatory nucleic acids useful according to the invention include standard viral and bacterial vectors, many of which are commercially available. In its broadest sense, a "vector" is any nucleic acid material which is ordinarily used to deliver and facilitate the transfer of nucleic acids to cells. The vector as used herein may be an empty
 5 vector or a vector carrying a gene which can be expressed. In the case when the vector is carrying a gene the vector generally transports the gene to the target cells with reduced degradation relative to the extent of degradation that would result in the absence of the vector. In this case the vector optionally includes gene expression sequences to enhance expression of the gene in target cells such as immune cells, but it is not required that the gene
 10 be expressed in the cell.

Nucleic acid-binding fragments of TLRs are believed to include the extracytoplasmic (extracellular) domain or subportions thereof, such as those which include at least an MBD motif, a CXXC motif, or both an MBD motif and a CXXC motif.

Both mouse and human TLR9 have an N-terminal extension of approximately 180
 15 amino acids compared to other TLRs. An insertion also occurs at amino acids 253-268, which is not found in TLRs 1-6 but is present in human TLR7 and human TLR8. This insert has two CXXC motifs which participate in forming a CXXC domain. The CXXC domain resembles a zinc finger motif and is found in DNA-binding proteins and in certain specific CpG binding proteins, e.g., methyl-CpG binding protein-1 (MBD-1). Fujita N et al. (2000)
 20 *Mol Cell Biol* 20:5107-18. Both human and mouse TLR9 CXXC domains occur at aa 253-268:

CXXC motif:	GNCXXCXXXXXXXXCXXC	SEQ ID NO:62
Human TLR9:	GNCRRCDHAPNPCMEC	SEQ ID NO:63
25 Murine TLR9:	GNCRRCDHAPNPCMIC	SEQ ID NO:64

An additional motif believed to be involved in CpG binding is the MBD motif, also found in MBD-1, listed below as SEQ ID NO:53. Fujita, N et al.(2000) *Mol Cell Biol* 20:5107-18; Ohki I et al. (1999) *EMBO J* 18:6653-61. Amino acids 524-554 of hTLR9 and
 30 aa 525-555 of mTLR9 correspond to the MBD motif of MBD-1 as shown:

MBD motif:

- 36 -

MBD-1	R-XXXXXXXX-R-X-D-X-Y-XXXXXXXXXX-R-S-XXXXXX-Y	SEQ ID NO:65
hTLR9	Q-XXXXXXXX-K-X-D-X-Y-XXXXXXXXXX-R-L-XXXXXX-Y	SEQ ID NO:66
mTLR9	Q-XXXXXXXX-K-X-D-X-Y-XXXXXXXXXX-Q-L-XXXXXX-Y	SEQ ID NO:67
5 hTLR9	Q-VLDLSRN-K-L-D-L-Y-HEHSFTELP-R-L-EALDLS-Y	SEQ ID NO:68
mTLR9	Q-VLDLSHN-K-L-D-L-Y-HWKSFSLEP-Q-L-QALDLS-Y	SEQ ID NO:69

Although the signaling functions of MBD-1 and TLR9 are quite different, the core D-X-Y is conserved and is believed to be involved in CpG binding.

10 According to another aspect of the invention, a screening method is provided for identifying an immunostimulatory compound. The method according to this aspect of the invention involves contacting a functional TLR9 with a test compound; detecting presence or absence of a response mediated by a TLR9 signal transduction pathway in the presence of the test compound arising as a result of an interaction between the functional TLR9 and the test
15 compound; and determining the test compound is an immunostimulatory compound when the presence of a response mediated by the TLR9 signal transduction pathway is detected.

An immunostimulatory compound is a natural or synthetic compound that is capable of inducing an immune response when contacted with an immune cell. A TLR9 ligand that is an immunostimulatory compound is a natural or synthetic compound that is capable of
20 inducing an immune response when contacted with an immune cell that expresses TLR9. A TLR9 ligand that is an immunostimulatory compound is also a natural or synthetic compound that is capable of inducing a TLR/IL-1R signal transduction pathway when contacted with a TLR9. Immunostimulatory compounds include but are not limited to immunostimulatory nucleic acids. The immunostimulatory compound can be, for example, a nucleic acid
25 molecule, polynucleotide or oligonucleotide, a polypeptide or oligopeptide, a lipid or lipopolysaccharide, a small molecule.

A basis for certain of the screening assays is the presence of a functional TLR9 in a cell. The functional TLR9 in some instances is naturally expressed by a cell. In other instances, expression of the functional TLR9 can involve introduction or reconstitution of a
30 species-specific TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact with an

- 37 -

immunostimulatory nucleic acid. In yet other instances, expression of the functional TLR9 can involve introduction of a chimeric or modified TLR9 into a cell or cell line that otherwise lacks the TLR9 or lacks responsiveness to immunostimulatory nucleic acid, resulting in a cell or cell line capable of activating the TLR/IL-1R signaling pathway in response to contact
5 with an immunostimulatory nucleic acid. Examples of cell lines lacking TLR9 or immunostimulatory nucleic acid responsiveness include, but are not limited to, 293 fibroblasts (ATCC CRL-1573), MonoMac-6, THP-1, U937, CHO, and any TLR9 knock-out. The introduction of the species-specific, chimeric or modified TLR9 into the cell or cell line is preferably accomplished by transient or stable transfection of the cell or cell line with a
10 TLR9-encoding nucleic acid sequence operatively linked to a gene expression sequence (as described above). Methods for transient and for stable transfection of a cell are well known in the art.

The screening assays can have any of a number of possible readout systems based upon either TLR/IL-1R signaling pathway or other assays useful for assessing response to
15 immunostimulatory nucleic acids. It has been reported that immune cell activation by CpG immunostimulatory sequences is dependent in some way on endosomal processing.

In certain embodiments, the readout for the screening assay is based on the use of native genes or, alternatively, cotransfected or otherwise co-introduced reporter gene constructs which are responsive to the TLR/IL-1R signal transduction pathway involving
20 MyD88, TRAF, p38, and/or ERK. Häcker H et al. (1999) *EMBO J* 18:6973-6982. These pathways activate kinases including κ B kinase complex and c-Jun N-terminal kinases. Thus reporter genes and reporter gene constructs particularly useful for the assays can include a reporter gene operatively linked to a promoter sensitive to NF- κ B. Examples of such promoters include, without limitation, those for NF- κ B, IL-1 β , IL-6, IL-8, IL-12 p40, CD80,
25 CD86, and TNF- α . The reporter gene operatively linked to the TLR-sensitive promoter can include, without limitation, an enzyme (e.g., luciferase, alkaline phosphatase, β -galactosidase, chloramphenicol acetyltransferase (CAT), etc.), a bioluminescence marker (e.g., green-fluorescent protein (GFP, U.S. Pat. No. 5,491,084), blue fluorescent protein, etc.), a surface-expressed molecule (e.g., CD25), and a secreted molecule (e.g., IL-8, IL-12 p40, TNF- α). In
30 certain embodiments the reporter is selected from IL-8, TNF- α , NF- κ B-luciferase (NF- κ B-luc; Häcker H et al. (1999) *EMBO J* 18:6973-6982), IL-12 p40-luc (Murphy TL et al. (1995)

- 38 -

Mol Cell Biol 15:5258-5267), and TNF-luc (Häcker H et al. (1999) *EMBO J* 18:6973-6982). At least one of these reporter constructs (NF- κ B-luc) is commercially available (Stratagene, La Jolla, CA). In assays relying on enzyme activity readout, substrate can be supplied as part of the assay, and detection can involve measurement of chemiluminescence, fluorescence, color development, incorporation of radioactive label, drug resistance, or other marker of enzyme activity. For assays relying on surface expression of a molecule, detection can be accomplished using FACS analysis or functional assays. Secreted molecules can be assayed using enzyme-linked immunosorbent assay (ELISA) or bioassays. Many such readout systems are well known in the art and are commercially available.

According to one embodiment of this method, comparison can be made to a reference immunostimulatory nucleic acid. The reference immunostimulatory nucleic acid may be any suitably selected immunostimulatory nucleic acid, including a CpG nucleic acid. In certain embodiments the screening method is performed using a plurality of test nucleic acids. In certain embodiments comparison of test and reference responses is based on comparison of quantitative measurements of responses in each instance.

In another aspect the invention provides a screening method for identifying species specificity of an immunostimulatory nucleic acid. The method involves contacting a TLR9 of a first species with a test immunostimulatory nucleic acid; contacting a TLR9 of a second species with the test immunostimulatory nucleic acid; measuring a response mediated by a TLR signal transduction pathway associated with the contacting the TLR9 of the first species with the test immunostimulatory nucleic acid; measuring a response mediated by the TLR signal transduction pathway associated with the contacting the TLR9 of the second species with the test immunostimulatory nucleic acid; and comparing the two responses. The TLR9 may be expressed by a cell or it may be part of a cell-free system. The TLR9 may be part of a complex, with either another TLR or with another protein, e.g., MyD88, IRAK, TRAF, I κ B, NF- κ B, or functional homologues and derivatives thereof. Thus for example a given ODN can be tested against a panel of human fibroblast 293 fibroblast cells transfected with TLR9 from various species and optionally cotransfected with a reporter construct sensitive to TLR/IL-1R activation pathways. Thus in another aspect, the invention provides a method for screening species selectivity with respect to a given nucleic acid sequence.

Test compounds can include but are not limited to peptide nucleic acids (PNAs), antibodies, polypeptides, carbohydrates, lipids, hormones, and small molecules. Test

- 39 -

compounds can further include variants of a reference immunostimulatory nucleic acid incorporating any one or combination of the substitutions described above. Test compounds can be generated as members of a combinatorial library of compounds.

In preferred embodiments, the screening methods can be performed on a large scale and with high throughput by incorporating, e.g., an array-based assay system and at least one automated or semi-automated step. For example, the assays can be set up using multiple-well plates in which cells are dispensed in individual wells and reagents are added in a systematic manner using a multiwell delivery device suited to the geometry of the multiwell plate. Manual and robotic multiwell delivery devices suitable for use in a high throughput screening assay are well known by those skilled in the art. Each well or array element can be mapped in a one-to-one manner to a particular test condition, such as the test compound. Readouts can also be performed in this multiwell array, preferably using a multiwell plate reader device or the like. Examples of such devices are well known in the art and are available through commercial sources. Sample and reagent handling can be automated to further enhance the throughput capacity of the screening assay, such that dozens, hundreds, thousands, or even millions of parallel assays can be performed in a day or in a week. Fully robotic systems are known in the art for applications such as generation and analysis of combinatorial libraries of synthetic compounds. See, for example, U.S. Pat. Nos. 5,443,791 and 5,708,158.

The following examples are provided for illustrative purposes and are not meant to be limiting in any way.

Examples

Example 1. Cloning and Sequencing of Rat, Porcine, Bovine, Equine, Ovine, Canine, and Feline TLR9

Cells and Tissues. Lymphoid tissues, primarily spleen or blood mononuclear cells (PBMC) from five mammalian species were collected: mouse, pig, bovine, rat and horse. Spleen samples were collected in RNeasyTM (Ambion[®], Austin, TX, USA), stabilized at 4°C overnight and stored at -70°C. Blood samples were centrifuged at 500 x g for 25 min at room temperature and the buffy coat, containing enriched PBMC, was then removed and stored at -70°C. The mouse specimen was used as a comparative positive control.

- 40 -

First-strand cDNA synthesis. Total RNA from the spleen and PBMC samples was isolated using a monophasic solution of phenol and guanidine isothiocyanate: TRIzol™ reagent (GIBCO BRL®, Burlington, ON, Canada) according to the manufacturer's instructions. First-strand cDNA was synthesized from the total RNA using
5 SUPERScript™ II reverse transcriptase (GIBCO BRL®, Burlington, ON, Canada). Approximately 3 µg of total RNA was added to 50 pmoles of oligo(dT) primer [poly T₍₁₈₎]; the mixture was heated to 70°C for 10 min and subsequently chilled on ice. The following was added to the cooled reaction mixture: 1 µl of mixed dNTP stock containing 10 mM each dATP, dCTP, dGTP and dTTP (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) at
10 neutral pH, 1X first strand buffer (50 mM Tris-HCl pH 8.3/ 75 mM KCl/ 3 mM MgCl₂) and 2 µl of 0.1 M DTT. The mixture was subsequently heated to 42°C for 2 min, followed by addition of 200 units of SUPERScript™ II reverse transcriptase. The reaction was carried out at 42°C for 50 min, followed by 70°C for 15 min. The first-strand cDNA was used as the template for subsequent polymerase chain reaction (PCR) amplifications.

15 *PCR amplification.* TLR9 gene was PCR amplified from each of the above-mentioned species using primers designed from known mouse and human TLR9 sequence in Genbank: Accession AF314224 and AF259262, respectively. The primers were designed using the primer design software, Clone Manager 5 (Scientific and Educational Software, Durham, NC, USA). TLR9 gene-specific primers used were:

20 forward primer 5'-ACCTTGCCTGCCTTCCTACCCTGTGA-3' (SEQ ID NO:37) and reverse primer 5'-GTCCGTGTGGGCCAGCACAAA-3' (SEQ ID NO:38).

The 2.7 Kbp fragment was PCR amplified using Advantage® 2 DNA polymerase mix (BD Biosciences Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. PCR reaction volumes of 25 µl contained 15 pmoles of each primer, 0.2 mM of dNTP mix
25 and 1 µl of reverse transcription reaction. PCR amplification was conducted by initial denaturation at 94°C for 1 min followed by 30 cycles of 94°C denaturation (15 sec), 65°C annealing (45 sec) and 72°C extensions (2 min), with a final extension at 72°C for 5 min.

Cloning and sequencing. The PCR amplified fragment was treated with 500 units of T4 DNA polymerase (Amersham Pharmacia Biotech Inc., Baie de Urfe, Quebec) for 15 min
30 at room temperature prior to cleaning the reaction with QIAquick PCR purification kit (QIAGEN Inc., Mississauga, ON, Canada). The fragment was then ligated to pZerO™ - 2

- 41 -

vector (Invitrogen™ Life Technologies, Burlington, ON, Canada), treated with *Eco RV* restriction enzyme, using T4 DNA Ligase (GIBCO BRL®, Burlington, ON, Canada). *E. coli* TOP 10 chemically competent cells (Invitrogen™ Life Technologies, Burlington, ON, Canada) were used to transform ligated products. Plasmids containing the 2.7 Kbp fragment were sequenced using an automated DNA sequencer, CEQ™ 2000XL DNA analysis system (Beckman Coulter Inc., Fullerton, CA, USA).

Sequences of the 2.7 Kbp fragment were derived from three clones of each species selected from independent PCR reactions to account for errors that may have been incurred during the PCR amplifications and to confirm the sequence data.

Nucleotide sequences of the rat, porcine, bovine, equine, ovine, canine, and feline TLR9 were extended and completed using standard 5' and 3' RACE PCR and primers designed using the sequences obtained from the 2.7 Kbp fragments.

Results. Nucleotide sequences of rat, porcine, bovine, equine, canine, and feline TLR9 cDNA obtained by the methods above are provided as SEQ ID NOs 3, 7, 11, 15, 19, 23, and 27, respectively. Deduced amino acid sequences are provided as SEQ ID NOs 1, 5, 9, 13, 17, 21, and 25, respectively. Deduced amino acid sequences of full-length murine and human TLR9 are provided as SEQ ID NOs 29 and 33, respectively.

Example 2. Comparison of Aligned Sequences for TLR9 from Various Mammalian Species.

Multiple sequence alignment of deduced amino acid sequences for feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 polypeptides was performed using Clustal W 1.82 (see, for example, www.cmbi.kun.nl/bioinf/tools/clustalw.shtml). In addition, paired sequence alignment of deduced amino acid sequences for murine and human TLR9 polypeptides was performed using Clustal W 1.82. The results of the multiple sequence alignment are presented in **Figure 1**. As will be appreciated from **Figure 1**, certain amino acids are highly conserved across all species examined. Similarly, certain amino acids differ only by conservative amino acid substitutions among the various species. In addition, it is evident that certain amino acids which are conserved between murine and human TLR9 are not conserved in other species. Furthermore, **Figure 1** also indicates that certain amino acids are highly divergent across various species. The information provided by the comparison of multiple species adds significantly to the information available by comparison between only murine and human TLR9 sequences.

- 42 -

The putative transmembrane regions of the TLR9 polypeptides are indicated in boxes in Figure 1. Sequence upstream of each transmembrane region is extracellular domain and is believed to include sequence primarily responsible for binding to TLR9 ligands, including CpG DNA. The extracellular domains of feline, canine, bovine, mouse, ovine, porcine, horse, human, and rat TLR9 correspond to amino acids numbered 1-820, 1-822, 1-818, 1-821, 1-818, 1-819, 1-820, 1-820, and 1-821, respectively, as shown in Figure 1.

Figure 2 presents an evolutionary relatedness tree for six TLR9 polypeptides examined. The cladogram in Figure 2 was prepared using Clustal W (see above). As can be appreciated from this figure, murine and human TLR9 are nearly the most divergent TLR9s in this group. Surprisingly, human and horse TLR9 appear relatively closely related.

Example 3. Reconstitution of TLR9 Signaling in 293 Fibroblasts.

Mouse TLR9 cDNA (SEQ ID NO:31) and human TLR9 cDNA (SEQ ID NO:35) in pT-Adv vector (from Clontech) were individually cloned into the expression vector pcDNA3.1(-) from Invitrogen using the EcoRI site. Utilizing a "gain of function" assay it was possible to reconstitute human TLR9 (hTLR9) and murine TLR9 (mTLR9) signaling in CpG-DNA non-responsive human 293 fibroblasts (ATCC, CRL-1573). The expression vectors mentioned above were transfected into 293 fibroblast cells using the calcium phosphate method.

Since NF- κ B activation is central to the IL-1/TLR signal transduction pathway (Medzhitov R et al. (1998) *Mol Cell* 2:253-258; Muzio M et al. (1998) *J Exp Med* 187:2097-101), cells were transfected with hTLR9 or co-transfected with hTLR9 and an NF- κ B-driven luciferase reporter construct. Human fibroblast 293 cells were transiently transfected with hTLR9 and a six-times NF- κ B-luciferase reporter plasmid (NF- κ B-luc) or with hTLR9 alone. After stimulus with CpG-ODN (2006, 2 μ M, TCGTCGTTTTGTCGTTTTGTCGTT, SEQ ID NO:58), GpC-ODN (2006-GC, 2 μ M, TGCTGCTTTTGTGCTTTTGTGCTT, SEQ ID NO:59), LPS (100 ng/ml) or media, NF- κ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results representative of three independent experiments showed that cells expressing hTLR9 responded to CpG-DNA but not to LPS.

Independently, human fibroblast 293 cells were transiently transfected with mTLR9 and the NF- κ B-luc construct or with mTLR9 alone. After stimulation with CpG-ODN (1668, 2 μ M; TCCATGACGTTTCCTGATGCT, SEQ ID NO:60), GpC-ODN (1668-GC, 2 μ M;

- 43 -

TCCATGAGCTTCCTGATGCT, SEQ ID NO:61), LPS (100 ng/ml) or media, NF- κ B activation by luciferase readout (8h) or IL-8 production by ELISA (48h) were monitored. Results showed that expression of TLR9 (human or mouse) in 293 cells results in a gain of function for CpG-DNA stimulation.

5 To generate stable clones expressing human TLR9, murine TLR9, or either TLR9 with the NF- κ B-luc reporter plasmid, 293 cells were transfected in 10 cm plates (2×10^6 cells/plate) with 16 μ g of DNA and selected with 0.7 mg/ml G418 (PAA Laboratories GmbH, Cölbe, Germany). Clones were tested for TLR9 expression by RT-PCR. The clones were also screened for IL-8 production or NF- κ B-luciferase activity after stimulation with
10 ODN. Four different types of clones were generated.

293-hTLR9-luc:	expressing human TLR9 and 6-fold NF- κ B-luciferase reporter
293-mTLR9-luc:	expressing murine TLR9 and 6-fold NF- κ B-luciferase reporter
293-hTLR9:	expressing human TLR9
15 293-mTLR9:	expressing murine TLR9

Results indicated that stable clones also responded to CpG-ODN.

Example 4. Similar ODN Sequence Specificity of TLR9 of Human and Equine TLR9.

20 3×10^6 293T cells were electroporated with 5 μ g NF- κ B-luc plasmid and 5 μ g of either horse TLR9-pcDNA3.1 plasmid or humanTLR9-pcDNA3.1 plasmid at 200V, 975 μ F. After the electroporation the cells were plated in 96-well cell culture plates at 2.5×10^4 cells per well and grown overnight at 37°C. The cells were stimulated with the indicated concentration of ODN for 16h, after which the supernatant was removed and the cells lysed in lysis buffer and
25 frozen for at least 2 hours at -80°C. Luciferase activity was measured by adding Luciferase Assay substrate from Promega. Values are given as fold specific induction over non-stimulated control. Results are shown in Figure 3.

As shown in Figure 3, ODN 2006 (TCGTCGTTTTGTCGTTTTGTCGTT; SEQ ID NO:58) has a strong specificity for human TLR9. ODN 1982
30 (TCCAGGACTTCTCTCAGGTT; SEQ ID NO:70) was the negative control ODN. ODN 5890 (TCCATGACGTTTTTTGATGTT; SEQ ID NO:39) has a strong specificity for mouse

- 44 -

TLR9. This experiment demonstrates the similarity of horse TLR9 to human TLR9 in binding specificity, a result predicted by the evolutionary relatedness of horse TLR9 to human TLR9. Mouse TLR9 is more distant from horse TLR9 and human TLR9 in sequence homology, and ODN 5890 was not detected by either human or horse TLR9.

5

Example 5. Non-human, Non-murine Native Mammalian TLR9 Useful in Screening for Human-Preferred CpG DNA.

Native rat, porcine, bovine, equine, and ovine TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Rat, porcine, bovine, equine, or ovine TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected native rat, porcine, bovine, equine, or ovine TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

20 Example 6. Chimeric TLR9 Useful in Screening for Human-Preferred CpG DNA.

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in this assay are then used as the basis for screening for additional human-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA.

30

Example 7. Chimeric TLR9 Responsive to Both Human-Preferred and Murine-Preferred CpG DNA.

- 45 -

Chimeric TLR9 polypeptides are screened for binding or TLR9 signaling activity when contacted with human-preferred CpG DNA (ODN 2006) and also screened for binding or TLR9 signaling activity when contacted with murine-preferred CpG DNA (ODN 1668). Chimeric TLR9 polypeptides which exhibit significant TLR9 binding or TLR9 signaling activity in each of these assays are then used as the basis for screening for additional human-preferred CpG DNA and for screening for additional murine-preferred CpG DNA. An expression vector containing a nucleic acid sequence encoding a selected chimeric TLR9 polypeptide, and optionally a reporter construct, is introduced into cells which do not express TLR9. The cells expressing the selected chimeric TLR9 polypeptide are contacted with candidate human-preferred CpG DNA or candidate murine-preferred CpG DNA. Candidate human-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as human-preferred CpG DNA. Candidate murine-preferred CpG DNA exhibiting significant TLR9 binding or TLR9 signaling activity are selected as murine-preferred CpG DNA.

Equivalents

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by examples provided, since the examples are intended as a single illustration of one aspect of the invention and other functionally equivalent embodiments are within the scope of the invention. Various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims. The advantages of the invention are not necessarily encompassed by each embodiment of the invention.

All references, patents and patent publications that are recited in this application are incorporated in their entirety herein by reference.

We claim:

- 46 -

Claims

1. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.

5

2. An isolated polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.

10

3. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13, and SEQ ID NO:17.

15

4. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:18.

5. A vector comprising the nucleic acid of any of claims 3-4.

6. A cell comprising the vector of claim 5.

20

7. An antibody or fragment thereof that binds specifically to the polypeptide of any of claims 1-2.

25

8. A method for identifying key amino acids in a TLR9 of a first species which confer specificity for CpG DNA optimized for TLR9 of the first species, comprising:

aligning protein sequences of TLR9 of a first species, TLR9 of a second species, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for TLR9 of the first species rather than when contacted with a CpG DNA optimized for TLR9 of the second species;

30

generating an initial set of candidate amino acids in the TLR9 of the first species by excluding each amino acid in the TLR9 of the first species which (a) is identical with the

- 47 -

TLR9 of the second species or (b) differs from the TLR9 of the second species only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the initial set of candidate amino acids in the TLR9 of the first species which (a) is identical with
5 the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in the TLR9 of the first species each amino acid in the refined set of candidate amino acids.

10 9. A method for identifying key amino acids in human TLR9 which confer specificity for CpG DNA optimized for human TLR9, comprising:

aligning protein sequences of human TLR9, murine TLR9, and TLR9 of a third species, wherein the TLR9 of the third species preferentially generates a signal when contacted with a CpG DNA optimized for human TLR9 rather than when contacted with a
15 CpG DNA optimized for murine TLR9;

generating an initial set of candidate amino acids in human TLR9 by excluding each amino acid in human TLR9 which (a) is identical with murine TLR9 or (b) differs from murine TLR9 only by conservative amino acid substitution;

generating a refined set of candidate amino acids by selecting each amino acid in the
20 initial set of candidate amino acids in human TLR9 which (a) is identical with the TLR9 of the third species or (b) differs from the TLR9 of the third species only by conservative amino acid substitution; and

identifying as key amino acids in human TLR9 each amino acid in the refined set of candidate amino acids.

25 10. The method according to claim 9, performed iteratively with a plurality of TLR9s derived from different species other than human and mouse, wherein for each TLR9 the refined set of candidate amino acids is assigned a weight, said weight corresponding to a ratio equal to (responsiveness to human-preferred CpG DNA)/(responsiveness to murine-preferred
30 CpG DNA).

- 48 -

11. An isolated polypeptide comprising an amino acid sequence identical to SEQ ID NO:30 except for substitution of at least one key amino acid identified according to the method of any of claims 9 or 10.

5 12. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide according to claim 11.

13. A vector comprising the nucleic acid of claim 12.

10 14. A cell comprising the vector of claim 13.

15. An antibody that binds specifically to the polypeptide of claim 14.

16. A screening method to identify a TLR9 ligand, comprising:
15 contacting a polypeptide according to any of claims 1, 2, or 11 with a candidate TLR9 ligand;
 measuring a signal in response to the contacting; and
 identifying the candidate TLR9 ligand as a TLR9 ligand when the signal in response to the contacting is consistent with TLR9 signaling.

20 17. The method of claim 16, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

25 18. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF- κ B.

19. The method of claim 17, wherein the candidate TLR9 ligand is an immunostimulatory nucleic acid.

30 20. The method of claim 19, wherein the immunostimulatory nucleic acid is CpG DNA.

- 49 -

21. A screening method to identify species-specific CpG-motif preference of an isolated polypeptide of claim 2 or claim 11, comprising:

contacting an isolated polypeptide of claim 2 or claim 11 with a CpG DNA comprising a hexamer sequence selected from the group consisting of GACGTT, AACGTT, CACGTT, TACGTT, GGCgTT, GCCGTT, GTCGTT, GATGTT, GAAGTT, GAGGTT, GACATT, GACCTT, GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA, and GACGTG;

measuring a signal in response to the contacting; and

identifying a species-specific CpG-motif preference when the signal in response to the contacting is consistent with TLR9 signaling.

22. The method of claim 21, wherein the signal comprises expression of a reporter gene responsive to TLR/IL-1R signal transduction pathway.

23. The method of claim 17, wherein the reporter gene is operatively linked to a promoter sensitive to NF- κ B.

24. The method of claim 21, wherein the CpG DNA is an oligodeoxynucleotide having a sequence selected from the group consisting of

20	TCCATGACGTTTTTGATGTT	(SEQ ID NO:39),
	TCCATAACGTTTTTGATGTT	(SEQ ID NO:40),
	TCCATCACGTTTTTGATGTT	(SEQ ID NO:41),
	TCCATTACGTTTTTGATGTT	(SEQ ID NO:42),
	TCCATGGCGTTTTTGATGTT	(SEQ ID NO:43),
25	TCCATGCCGTTTTTGATGTT	(SEQ ID NO:44),
	TCCATGTCGTTTTTGATGTT	(SEQ ID NO:45),
	TCCATGATGTTTTTGATGTT	(SEQ ID NO:46),
	TCCATGAAGTTTTTGATGTT	(SEQ ID NO:47),
	TCCATGAGGTTTTTGATGTT	(SEQ ID NO:48),
30	TCCATGACATTTTTGATGTT	(SEQ ID NO:49),
	TCCATGACCTTTTTGATGTT	(SEQ ID NO:50),
	TCCATGACTTTTTTGATGTT	(SEQ ID NO:51),
	TCCATGACGCTTTTGATGTT	(SEQ ID NO:52),
	TCCATGACGATTTTGATGTT	(SEQ ID NO:53),
35	TCCATGACGGTTTTGATGTT	(SEQ ID NO:54),
	TCCATGACGTCTTTGATGTT	(SEQ ID NO:55),
	TCCATGACGTATTTGATGTT	(SEQ ID NO:56), and
	TCCATGACGTGTTTGATGTT	(SEQ ID NO:57).

Figure 1
(1/3)

feline	MGPCRGALHPLSLLVQAAALAVALAAGTLPAPFLPCELPQPHGLVNCNWFLFLKSVPHFSAAA	60
canine	MGPCRGALHPLSLLVQAAALALALAAGTLPAPFLPCELPQPHGLVNCNWFLFLKSVPHFSAAA	60
bovine	MGP-YCAPHPLSLLVQAAALAAALAEAGTLPAPFLPCELPQPHGQVDCNWFLFLKSVPHFSAGA	59
mouse	MGP-YCAPHPLSLLVQAAALAAALAEAGTLPAPFLPCELPQPHGQVDCNWFLFLKSVPHFSAGA	59
ovine	MGP-YCAPHPLSLLVQAAALAAALAEAGTLPAPFLPCELPQPHGQVDCNWFLFLKSVPHFSAGA	59
porcine	MGP-RCTLHPLSLLVQVTAALAAALAEAGTLPAPFLPCELPQPHGLVNCNWFLFLKSVPHFSAAA	59
horse	MGPCHGALQPLSLLVQAAMLAVALAAGTLPAPFLPCELPQPHGLVNCNWFLFLKSVPHFSAAA	60
human	MGFCSRSLHPLSLLVQAIMLAMTLALGTLPAPFLPCELPQPHGLVNCNWFLFLKSVPHFSMAA	60
rat	MVLCRRTLHPLSLLVQAAVLAELALGTLPAPFLPCELPKPHGLVDCNWFLFLKSVPHFSAAE	60
	* : :*****. ** : ** * ** .*****: ; * *.:*****.***	
feline	PRGNVTSLSLYSNRIHHLHDSDFVHLSSRLRLNLKWNCPASLSPMHFPCHMTIEPHTFL	120
canine	PRGNVTSLSLYSNRIHHLHDYDFVHFVHLRRLNLKWNCPASLSPMHFPCHMTIEPNTFL	120
bovine	PRANVTSLSLISNRIHHLHDSDFVHLNRLVNLKWNCPAGLSPMHFPCRMTIEPNTFL	119
mouse	PRANVTSLSLISNRIHHLHDSDFVHLNRLVNLKWNCPAGLSPMHFPCRMTIEPNTFL	119
ovine	PRANVTSLSLISNRIHHLHDSDFVHLNRLVNLKWNCPAGLSPMHFPCRMTIEPNTFL	119
porcine	PRANVTSLSLISNRIHHLHDSDFVHLNRLVNLKWNCPAGLSPMHFPCRMTIEPNTFL	119
horse	PRDNVTSLSLISNRIHHLHDSDFVHLSSRLRLNLKWNCPAGLSPMHFPCHMTIEPNTFL	119
human	PRGNVTSLSLISNRIHHLHDSDFVHLNRLVNLKWNCPAGLSPMHFPCHMTIEPNTFL	120
rat	PRSNITSLSLIANRIHHLHNLDFVHLNPNVRLNLKWNCPAGLSPMHFPCRMTIEPNTFL	120
	** *:***** :*****: **.: : : ***** .***:***:***** **	
feline	AVPTLEELNLSYNSITTPALPSSIVLSLSRSTNIIVLDPANLAGLSLRLFLDGNCCY	180
canine	AVPTLEELNLSYNSITTPALPSSIVLSLSRSTNIIVLDPANLAGLSLRLFLDGNCCY	180
bovine	AVPTLEELNLSYNGITTPALPSSIVLSLSRSTNIIVLDPATHGLHALRFLYMDGNCCY	179
mouse	AVPTLEELNLSYNGITTPALPSSIVLSLSRSTNIIVLDPATHGLHALRFLYMDGNCCY	179
ovine	AVPTLEELNLSYNGITTPALPSSIVLSLSRSTNIIVLDPATHGLHALRFLYMDGNCCY	179
porcine	AVPTLEELNLSYNSITTPALPSSIVLSLSRSTNIIVLDPATHGLHALRFLYMDGNCCY	179
horse	AVPTLEELNLSYNGITTPALPSSIVLSLSRSTNIIQLDPTSLTGLHALRFLYMDGNCCY	180
human	AVPTLEELNLSYNSITTPALPSSIVLSLSRSTNIIQLDPTSLTGLHALRFLYMDGNCCY	180
rat	AMRMLEELNLSYNGITTPALPSSIVLSLSRSTNIIQLDPTSLTGLHALRFLYMDGNCCY	180
	*: **:******.*** **.* **.* **.* **.* **.* **.* **.* **.* **.*	
feline	KNPCQALQVAPGALLGLGNLTHLSLKYNLTAVERGLPSSLEYLLSYNHIITLAPEDL	240
canine	KNPCQALQVAPGALLGLGNLTHLSLKYNLTVVERGLPSSLEYLLSYNHIITLAPEDL	240
bovine	MNCPRALEVAPGALLGLGNLTHLSLKYNLTVVERGLPSSLEYLLSYNHIITLAPEDL	239
mouse	MNCPRALEVAPGALLGLGNLTHLSLKYNLTVVERGLPSSLEYLLSYNHIITLAPEDL	239
ovine	KNPCQAVEVAPGALLGLGNLTHLSLKYNLTVVERGLPSSLEYLLSYNHIITLAPEDL	239
porcine	KNPCQALEVVPAGALLGLGNLTHLSLKYNLTVVERGLPSSLEYLLSYNHIITLAPEDL	239
horse	KNPCGRALEVAPGALLGLGNLTHLSLKYNLTVVERGLPSSLEYLLSYNHIITLAPEDL	240
human	KNPCQALEVAPGALLGLGNLTHLSLKYNLTVVERGLPSSLEYLLSYNHIITLAPEDL	240
rat	KNPCNGAVNVTDAFLGLSNLTHLSLKYNLTVVERGLPSSLEYLLSYNHIITLAPEDL	240
	*** *:***.***:*****.***** **.* **.*: ***** *:*** **.*	
feline	ANLTALRVLDVGGNCRRCDHARNPCMECPKGFPHLPDFTFHLNHLGLVLDKSSLYNLN	300
canine	ANLTALRVLDVGGNCRRCDHARNPCRECPKGFQPLHPDFTFHLNHLGLVLDKSSLYSLD	300
bovine	ANLTALRVLDVGGNCRRCDHARNPCRECPKGFPHLPDFTFHLNHLGLVLDKSSLYKLE	299
mouse	ANLTALRVLDVGGNCRRCDHARNPCRECPKGFPHLPDFTFHLNHLGLVLDKSSLYKLE	299
ovine	ANLTALRVLDVGGNCRRCDHARNPCRECPKGFPHLPDFTFHLNHLGLVLDKSSLYKLE	299
porcine	ANLTALRVLDVGGNCRRCDHARNPCRECPKGFPHLPDFTFHLNHLGLVLDKSSLYNLD	299
horse	ANLTALRVLDVGGNCRRCDHARNPCVECPKGFPHLPDFTFHLNHLGLVLDKSSLYQLN	300
human	ANLTALRVLDVGGNCRRCDHARNPCMECPKGFQPLHPDFTFHLNHLGLVLDKSSLYSLN	300
rat	ANLTSLRMLDVGGNCRRCDHAPDLCTECRQKSLDLHPDFTFHLNHLGLVLDKSSLYSLN	300
	****:***:*****.***** : * ** : .***:*** **.*:*****.*** *	
feline	PRWFHALGNLMVLDLSENFLYDCITKTTFQGLAQLRLNLNLSFNYHKKVSFAHLHLAPSF	360
canine	PRWFHGLGNLMVLDLSENFLYDCITKTTFQGLAQLRLNLNLSFNYHKKVSFAHLHLASSF	360
bovine	KDWFRGLGRQLVLDLSENFLYDYITKTTFIENDLTQLRLNLNLSFNYHKKVSFAHLHLASSF	359
mouse	KDWFRGLGRQLVLDLSENFLYDYITKTTFIENDLTQLRLNLNLSFNYHKKVSFAHLHLASSF	359
ovine	KDWFRGLGRQLVLDLSENFLYDYITKTTFIENDLTQLRLNLNLSFNYHKKVSFAHLHLAPSF	359
porcine	TRWFRGLDRQLVLDLSENFLYDCITKTTFQGLAQLRLNLNLSFNYHKKVSFAHLHLAPSF	359
horse	PRWFRGLGNLTVLDLSENFLYDCITKTTFQGLAQLRLNLNLSFNYHKKVSFAHLHLAPSF	360
human	ASWFRGLGNLTVLDLSENFLYKCTKTTFQGLAQLRLNLNLSFNYHKKVSFAHLHLAPSF	360
rat	SKWFRGLANLTVLDLSENFLYESINKTSAFQNLTRLRLKDLNLSFNYHKKVSFAHLHLASSF	360
	:* * ** **.* **.* ***** **.* **.* ***** **.*	

Figure 1
(2/3)

feline	GSLLSLQQLDMHGIFFRSLSETTLRSLVHLPLMLQSLHLMQNFINQAQLSIFGAFPGRLRYV	420
canine	GSLLSLQELDIHGIFFRSLSKTTLQSLAHLPLMLQRHLQLNFIQAQLSIFGAFPGRLRYV	420
bovine	GSLVSLEKLDMHGIFFRSLTNITLQSLTRLPKLQSLHLMQNFINQAQLSIFGAFPSLLFV	419
mouse	GSLVSLEKLDMHGIFFRSLTNITLQSLTRLPKLQSLHLMQNFINQAQLSIFGAFPSLLFV	419
ovine	GGLVSLEKLDMHGIFFRSLTNTTLRPLTQLPKLQSLSLQLNFINQAELSIFGAFPSLLFV	419
porcine	GHLRSLKELDMHGIFFRSLSETTLQPLVQLPMLQTLLRMQNFINQAQLSIFGAFPGLLYV	419
horse	GSLLSLQELDMHGIFFRSLSQKTLOPLARLPMLQRLYLQMNFINQAQLGIKFDPGLRYI	420
human	GSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGFRAFPPGLRYV	420
rat	KSLVSLQELNMNGIFFRLNKNTLRWLAGLPKLHTLRLQMNFINQAQLSVFTFRALRFV	420
	* :*:~*::***** * : ~*: * . ** *: * ~*:***.***::~* * . * ::	

feline	DLSDNRISGAMELAAATGEVDG--GERVRLPSGDLALGPPGTPSSEGFMPGCKTLNFTLD	478
canine	DLSDNRISGAEPAAATGEVEADCGERVWPQSRDLALGPLGTPGSEAFMPSCRTLNFTLD	480
bovine	DLSDNRISGAATPAAALGEVDS--RVEVWRLPRGLAPGPLDAVSSKDFMPSCN-LNFTLD	476
mouse	DLSDNRISGAATPAAALGEVDS--RVEVWRLPRGLAPGPLDAVSSKDFMPSCN-LNFTLD	476
ovine	DLSDNRISGAARPVAALGEVDS--GVEVWRWPRGLAPGPLAAVSAKDFMPSCN-LNFTLD	476
porcine	DLSDNRISGAARPVAITREVDG--RERVWLPSRNLAPRPLDLTARSEDFMPNCKAFSFTLD	477
horse	DLSDNRISGAVEPVATTGEVDG--GKKVWLTSRDLTGPGLDTPSSEDFMPSCNLSFTLD	478
human	DLSDNRISGASELTATMGEADG--GEKVWLQPGDLAPAPVDTPSSEDFRPNCSLTNFTLD	478
rat	DLSDNRISGPPTLSRVAPEKAD-EAEKGVPWPASLTALPSTPVSKNFMVRCKNLRFMTMD	479
	:** * . . .*: : : : * * : **:*	

feline	LSRNNLVTTIQPEMFARLSRLQCLLSRNSISQAVNGSQFMPPLTSLQVLDLSHNKLDLYHG	538
canine	LSRNNLVTVQPEMFVRLARLQCLGLSHNSISQAVNGSQFVPLSNLRVLDLSHNKLDLYHG	540
bovine	LSRNNLVTTIQQEMFTRLRLQCLRLSHNSISQAVNGSQFVPLTSLRVLDLSHNKLDLYHG	536
mouse	LSRNNLVTTIQQEMFTRLRLQCLRLSHNSISQAVNGSQFVPLTSLRVLDLSHNKLDLYHG	536
ovine	LSRNNLVTTIQQEMFTRLRLQCLRLSHNSISQAVNGSQFVPLTSLRVLDLSYNKLDLYHG	536
porcine	LSRNNLVTTIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVLDLSHNKLDLYHG	537
horse	LSRNNLVTVQPEMFAQLSRLQCLRLSHNSISQAVNGSQFVPLTSLQVLDLSHNKLDLYHG	538
human	LSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFPLPTGLQVLDLSHNKLDLYHG	538
rat	LSRNNQVTIKPEMFVNLSHLQCLSLSHNCIAQAVNGSQFPLPTNLKVLDLSYNKLDLYHS	539

feline	RSFTFLPRLEALDLSYNSQPFMSMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQQLCSA	598
canine	RSFTFLPRLEALDLSYNSQPFMSMRGVGHNLSFVAQLPALRYLSLAHNIGHSRVSQQQLRSA	600
bovine	RSFTFLPQLEALDLSYNSQPFMSMQGVGHNLSFVAQLPSLRYS LAHNIGHSRV SQKLSSA	596
mouse	RSFTFLPQLEALDLSYNSQPFMSMQGVGHNLSFVAQLPSLRYS LAHNIGH SRVS QK LSSA	596
ovine	RSFTFLPQLEALDLSYNSQPFMSMQGVGHNLSFVAQLPSLRYS LAHNIGH SRVS QK LSSA	596
porcine	RSFTFLPRLEALDLSYNSQPFTMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQQLCSA	597
horse	RSFTFLPRLEALDLSYNSQPFMSMRGVGHNLSFVAQLPTLRLYS LAHNIGH SRVS QQ LCST	598
human	HSTFTFLPRLEALDLSYNSQPFMGVGHNFSFAHLRTLRLHSLAHNNIHQS QSQC LST	598
rat	KSFSELPQLQALDLSYNSQPFMSGIGHNFSFLANLSRLQNLSLAHNDIHSRVSSRLYST	599
	.*:***** *:*****: * :*****.****.:* *:.	

feline	SLRALDFSGNALSRLMWAEGDLYLHFFRGLRSLVRLDLSQNRLHTLLPRTLNLPKSLRL	658
canine	SLRALDFSGNTLSQMWAEGLDYLRFQGLRSLVQLDLSQNRLHTLLPRNLNLPKSLRL	660
bovine	SLRALDFSGNSLSQMWAEGLDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLNLPKSLRQL	656
mouse	SLRALDFSGNSLSQMWAEGLDLYLCFFKGLRNLVQLDLSENHLHTLLPRHLNLPKSLRQL	656
ovine	SLRALDFSGNSLSQMWAEGLDLYLCFFKGLRNLVQLDLSKNHLHTLLPRHLNLPKSLRQL	656
porcine	SLCALDFSGNDLSRLMWAEGDLYLRFQGLRSLVWLDLSQNLHTLLPRALNLPKSLKHL	657
horse	SLWALDFSGNSLSQMWAEGLDYLRFQGLRSLIRLDLSQNRLHTLLPCTLGNLPKSLQL	658
human	SLRALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSQNRLHTLLPQTLRNLPKSLQVL	658
rat	SVEYLDMSGNGVGRMWDEEDLYLYFFQDLRSLIHLDLSQNKHLHLRFQNLNLYLPKSLTKL	659
	*: ***** *: * * * * * *: * *: *****: * * * * * * * * * * *	

feline	RLRDNYLAFFNWSSSLVLLPRLEALDLAGNQLKALSNGSLPNGTQLQRDLSSNSISFVAS	718
canine	RLRDNYLAFFNWSSSLALLPKLEALDLAGNQLKALSNGSLPNGTQLQRDLSGNSIGFVVP	720
bovine	RLRDNNLAFFNWSSSLTVLPRLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIP	716
mouse	RLRDNNLAFFNWSSSLTVLPRLEALDLAGNQLKALSNGSLPPGIRLQKLDVSSNSIGFVIP	716
ovine	RLRDNNLAFFNWSSSLTVLPQLEALDLAGNQLKALSNGSLPPGTRLQKLDVSSNSIGFVTP	716
porcine	RLRDNNLAFFNWSSSLTLLPKLETLDLAGNQLKALSNGSLPSGTQLRRDLSGNSIGFVNP	717
horse	RLRNNYLAFFNWSSSLTLLPNLETLDLAGNQLKALSNGSLPSGTQLQRLDVSRNSIIFVVP	718
human	RLRDNYLAFFKWWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFVAP	718
rat	SFRDNHLSFFNWSSSLAFLPNLRDLDLAGNLLKALTNGTLPNGTLLQKLDVSSNSIVFVVP	719
	*** **	

Figure 1
(3/3)

feline	SFFALATRLRELNLNSANALKTVEPSWFGSLAGTLKVLVDVTGNPLHCACGAAFVDFLLEVO	778
canine	SFFALAVRLRELNLNSANALKTVEPSWFGSLAGALKVLDTANPLHCACGATFVDFLLEVO	780
bovine	GFFVRATRLIELNLNSANALKTVDPWSWFGSLAGTLKILDV SANPLHCACGA AFVDFLLERQ	776
mouse	GFFVRATRLIELNLNSANALKTVDPWSWFGSLAGTLKILDV SANPLHCACGA AFVDFLLERQ	776
ovine	GFFVLANRLKELNLNSANALKTVDPFWFGRLTETLNILDVSANPLHCACGA AFVDFLLEMQ	776
porcine	GFFALAKQLEELNLNSANALKTVEPSWFGSMVG NLKVLDVSANPLHCACGATFVGFLLEVO	777
horse	GFFALATRLRELNLNSANALRTEEP SWFGFLAGSLLEVLDVSANPLHCACGA AFVDFLLQVO	778
human	GFFSKAKELRELNLNSANALKTV DHSWFGPLASALQILDVSANPLHCACGA AFMDFLLEVO	778
rat	AFFALAVELKEVNLSHNILKTVD RSWFGPIVMNLTVL DVSSNPLHCACGA PFVDLLEVO	779
	. ** * . * *:*** * *: : *** :. * :***:*****.*.:*: *	
feline	AAVPGLPGHV KCGSPGQLQGRSIFAQDLRLCLDEALS WDCFG	838
canine	AAVPGLPSRVKCGSPGQLQGRSIFAQDLRLCLDEALS WVCFS	840
bovine	EAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLS LDCFG	836
mouse	EAVPGLSRRVTCGSPGQLQGRSIFTQDLRLCLDETLS LDCFG	836
ovine	AAVPGLSRRVTCGSPGQLQGRSIFAQDLRLCLDETLS LDCFG	836
porcine	AAVPGLPSRVKCGSPGQLQGHSIFAQDLRLCLDETLS WNCFG	837
horse	AAVPGLPSRVKCGSPGQLQGRSIFAQDLRLCLDKSL S WDCFG	838
human	AAVPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALS WDCFA	838
rat	TKVPGLANGVKCGSPRQLQGRSIFAQDLRLCLDDVLS RDCFG	839
	****. *.***** **** **:*****. ** *.**:*** :*. :*:** :	
feline	CGWDLWYCFHLCLAWLP RRGR--RGADALPYDAFVV FDKAQS AVADWVYNELRVRL EER	896
canine	CGWDLWYCFHLCLAWLP RRGR--RGVDALAYDAFVV FDKAQSS VADWVYNELRVQLEER	898
bovine	CGWDLWYCFHLCLAHLPRRRRQ--RGEDTLLYDAVVVF DKVQSAVADWVYNELRVQLEER	894
mouse	CGWDLWYCFHLCLAHLPRRRRQ--RGEDTLLYDAVVVF DKVQSAVADWVYNELRVQLEER	894
ovine	CGWDLWYCFHLCLAHLPRRRRQ--RGEDTLLYDAFVV FDKAQS AVADWVYNELRVQLEER	894
porcine	CGWDLWYCFHLCLAWLP HRGQR--RGADALFYDAFVV FDKAQS AVADWVYNELRVQLEER	895
horse	CGWDLWYCFHLGLAWLP RRGWQ--RGADALS YDAFVV FDKAQS AVADWVYNELRVRL EER	896
human	CGWDLWYCFHLCLAWLPWRGSRGRDEDALPYDAFVV FDKTQSAVADWVYNELRGQLEEC	898
rat	CGWDVWYCFHLCLAWLP LLTRGR-RSAQALPYDAFVV FDKAQS AVADWVYNELRVRL EER	898
	:** ** ** *. ::* ***.*****.*:*****:***	
feline	RGRRALRLCLEERDWP GKT LFENLWASVY SSRKMLFVL AHTDRVSGLLRAS FL LAQQRL	956
canine	RGRRALRLCLEERDWP GKT LFENLWASVY SRKTLFVL AHTDRVSGLLRAS FL LAQQRL	958
bovine	RGRRALRLCLEERDWP GKT LFENLWASVY SRKTMFVLD HTDRVSGLLRAS FL LAQQRL	954
mouse	RGRRALRLCLEERDWP GKT LFENLWASVY SRKTMFVLD HTDRVSGLLRAS FL LAQQRL	954
ovine	RGRRALRLCLEERDWP GKT LFENLWASVY SRKTMFVLD HTDRVSGLLRAS FL LAQQRL	954
porcine	RGRRALRLCLEERDWP GKT LFENLWASVY SRKTLFVL AHTDRVSGLLRAS FL LAQQRL	955
horse	RGRRALRLCLEERDWP GKT LFENLWASVY SRKMLFVL AHTDQVSGLLRAS FL LAQQRL	956
human	RGRWALRLCLEERDWP GKT LFENLWASVY SRKTLFVL AHTDRVSGLLRAS FL LAQQRL	958
rat	RGRRALRLCLED RDWP GQT LFENLWASIYSGRKTLFVL AHTDKVSGLLRAS FL LAQQRL	958
	*** *****:***:*.**:*****:*.*** :*** :*.**:*****:*****	
feline	LED RKDVVLV ILRP DAHRSRYVRLR QRLCRQSVLL WPHQP SGQRS FWA QLGTAL TRDNQ	1016
canine	LED RKDVVLV ILCP DAHRSRYVRLR QRLCRQSVLL WPHQP SGQRS FWA QLGTAL TRDNR	1018
bovine	LED RKDVVLV ILRP AAYSRYVRLR QRLCRQSVLL WPHQP SGQGS FWANLGIAL TRDNR	1014
mouse	LED RKDVVLV ILRP AAYSRYVRLR QRLCRQSVLL WPHQP SGQGS FWANLGIAL TRDNR	1014
ovine	LED RKDVVLV ILRP AAYSRYVRLR QRLCRQSVLL WPHQP SGQGS FWANLGIAL TRDNR	1014
porcine	LED RKDVVLV ILRP DAYRSRYVRLR QRLCRQSVLL WPHQP PRGQGS FWA QLGTAL TRDNH	1015
horse	LED RKDVVLV ILS PDARRSYVRLR QRLCRQSVLF WPHQP SGQRS FWA QLGMA LTRDNR	1016
human	LED RKDVVLV ILS PDGRRSYVRLR QRLCRQSVLL WPHQP SGQRS FWA QLGMA LTRDNH	1018
rat	LED RKDVVLV ILRP DAHRSRYVRLR QRLCRQSVLF WPHQP NGQGS FWA QLSTAL TRDNH	1018
	***** * . *****:*****:*** ** *****:*. *****:	
feline	HFYNQNFCRGPTTAE-----	1031
canine	HFYNQNFCRGPTTA-----	1032
bovine	HFYNRNFCRGPTTAE-----	1029
mouse	HFYNRNFCRGPTTAE-----	1032
ovine	HFYNRNFCRGPTTAE-----	1029
porcine	HFYNRNFCRGPTTAE-----	1030
horse	HFYNQNFCRGPTMAE-----	1031
human	HFYNRNFCQGPTAE-----	1032
rat	HFYNRNFCRGPTAE-----	1032
	*****.*****	

Figure 2

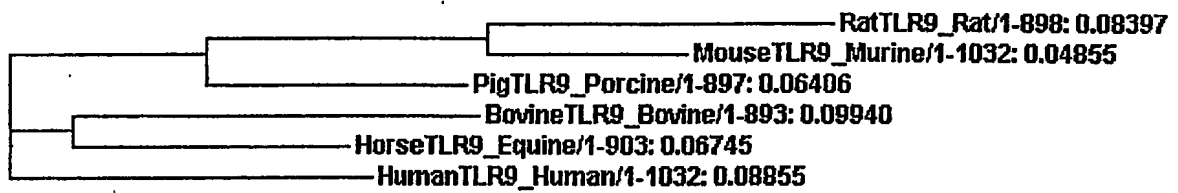
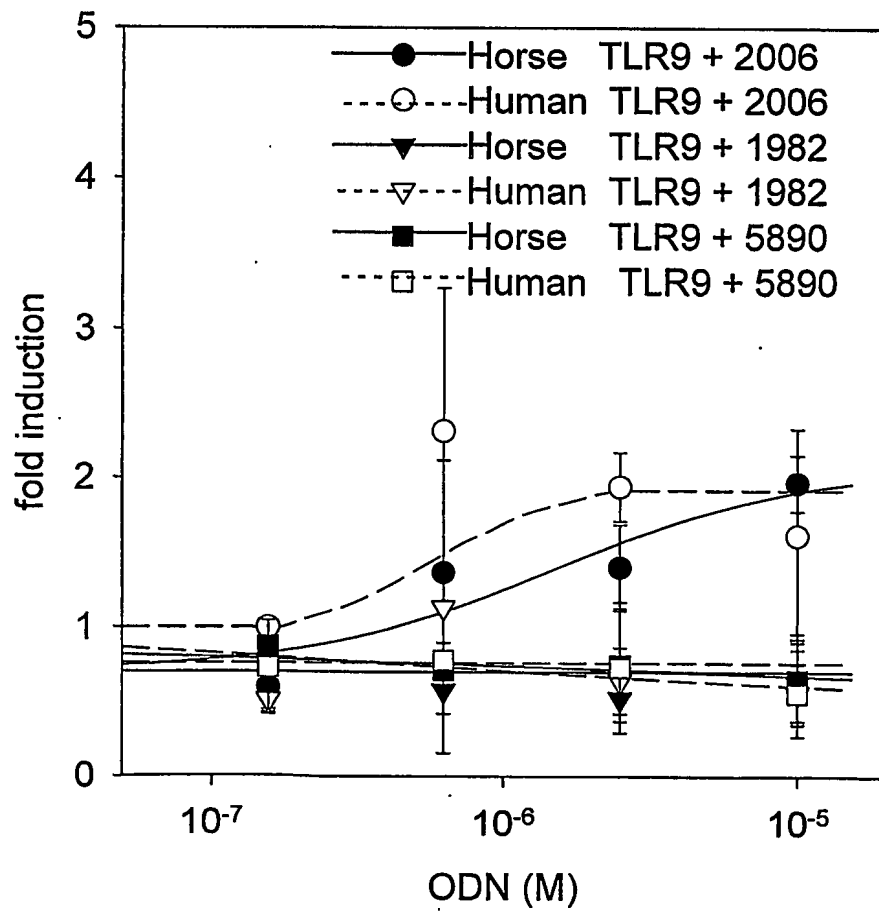


Figure 3



SEQUENCE LISTING

<110> Coley Pharmaceutical GmbH
University of Saskatchewan
Qiagen GmbH

<120> TOLL-LIKE RECEPTOR 9 (TLR9) FROM VARIOUS MAMMALIAN SPECIES

<130> C1041.70040WO00

<150> US 60/412,479

<151> 2002-09-19

<160> 70

<170> PatentIn version 3.1

<210> 1

<211> 1032

<212> PRT

<213> Rattus norvegicus

<400> 1

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn
50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn
65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met
100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
130 135 140

Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro
180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser
260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly
275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe
290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu
325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala
340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu
355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu
370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala
405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr
420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val
435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser
450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu
465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala
500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp
515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu
530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser
565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val
580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly
595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe

610					615					620					
Phe 625	Gln	Asp	Leu	Arg	Ser 630	Leu	Ile	His	Leu	Asp 635	Leu	Ser	Gln	Asn	Lys 640
Leu	His	Ile	Leu	Arg 645	Pro	Gln	Asn	Leu	Asn 650	Tyr	Leu	Pro	Lys	Ser	Leu
Thr	Lys	Leu	Ser 660	Phe	Arg	Asp	Asn	His 665	Leu	Ser	Phe	Phe	Asn 670	Trp	Ser
Ser	Leu	Ala 675	Phe	Leu	Pro	Asn	Leu 680	Arg	Asp	Leu	Asp 685	Leu	Ala	Gly	Asn
Leu	Leu 690	Lys	Ala	Leu	Thr	Asn 695	Gly	Thr	Leu	Pro	Asn 700	Gly	Thr	Leu	Leu
Gln 705	Lys	Leu	Asp	Val	Ser 710	Ser	Asn	Ser	Ile	Val 715	Phe	Val	Val	Pro	Ala 720
Phe	Phe	Ala	Leu	Ala 725	Val	Glu	Leu	Lys	Glu 730	Val	Asn	Leu	Ser	His 735	Asn
Ile	Leu	Lys	Thr 740	Val	Asp	Arg	Ser	Trp 745	Phe	Gly	Pro	Ile	Val 750	Met	Asn
Leu	Thr 755	Val	Leu	Asp	Val	Ser	Ser 760	Asn	Pro	Leu	His 765	Cys	Ala	Cys	Gly
Ala 770	Pro	Phe	Val	Asp	Leu	Leu 775	Leu	Glu	Val	Gln 780	Thr	Lys	Val	Pro	Gly
Leu 785	Ala	Asn	Gly	Val	Lys 790	Cys	Gly	Ser	Pro	Arg 795	Gln	Leu	Gln	Gly	Arg 800
Ser	Ile	Phe	Ala	Gln 805	Asp	Leu	Arg	Leu	Cys 810	Leu	Asp	Asp	Val	Leu	Ser
Arg	Asp	Cys 820	Phe	Gly	Leu	Ser	Leu 825	Leu	Ala	Val	Ala	Val	Gly 830	Thr	Val
Leu	Pro 835	Leu	Leu	Gln	His	Leu	Cys 840	Gly	Trp	Asp	Val	Trp 845	Tyr	Cys	Phe

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Thr Arg Gly Arg Arg Ser
 850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln
 865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu
 885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp
 900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr
 915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Lys Val Ser
 930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
 980 985 990

Leu Phe Trp Pro His Gln Pro Asn Gly Gln Gly Ser Phe Trp Ala Gln
 995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu
 1025 1030

<210> 2
 <211> 821
 <212> PRT
 <213> Rattus norvegicus

<400> 2

Met Val Leu Cys Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Val Leu Ala Glu Ala Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Glu Pro Arg Ser Asn
50 55 60

Ile Thr Ser Leu Ser Leu Ile Ala Asn Arg Ile His His Leu His Asn
65 70 75 80

Leu Asp Phe Val His Leu Pro Asn Val Arg Gln Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Pro Gly Leu Ser Pro Leu His Phe Ser Cys Arg Met
100 105 110

Thr Ile Glu Pro Lys Thr Phe Leu Ala Met Arg Met Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
130 135 140

Leu Thr Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
145 150 155 160

Ser Ser Leu Ala Gly Leu His Ser Leu Arg Val Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Asn Gly Ala Val Asn Val Thr Pro
180 185 190

Asp Ala Phe Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
195 200 205

Asn Asn Leu Thr Glu Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
210 215 220

Leu Leu Leu Ser Tyr Asn Leu Ile Val Lys Leu Gly Ala Glu Asp Leu
225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Met Leu Asp Val Gly Gly Asn Cys Arg
245 250 255

Arg Cys Asp His Ala Pro Asp Leu Cys Thr Glu Cys Arg Gln Lys Ser
 260 265 270

Leu Asp Leu His Pro Gln Thr Phe His His Leu Ser His Leu Glu Gly
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Ser Leu Asn Ser Lys Trp Phe
 290 295 300

Gln Gly Leu Ala Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Tyr Glu Ser Ile Asn Lys Thr Ser Ala Phe Gln Asn Leu Thr Arg Leu
 325 330 335

Arg Lys Leu Asp Leu Ser Phe Asn Tyr Cys Lys Lys Val Ser Phe Ala
 340 345 350

Arg Leu His Leu Ala Ser Ser Phe Lys Ser Leu Val Ser Leu Gln Glu
 355 360 365

Leu Asn Met Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Asn Thr Leu
 370 375 380

Arg Trp Leu Ala Gly Leu Pro Lys Leu His Thr Leu His Leu Gln Met
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Val Phe Ser Thr Phe Arg Ala
 405 410 415

Leu Arg Phe Val Asp Leu Ser Asn Asn Arg Ile Ser Gly Pro Pro Thr
 420 425 430

Leu Ser Arg Val Ala Pro Glu Lys Ala Asp Glu Ala Glu Lys Gly Val
 435 440 445

Pro Trp Pro Ala Ser Leu Thr Pro Ala Leu Pro Ser Thr Pro Val Ser
 450 455 460

Lys Asn Phe Met Val Arg Cys Lys Asn Leu Arg Phe Thr Met Asp Leu
 465 470 475 480

Ser Arg Asn Asn Gln Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
 485 490 495

Ser His Leu Gln Cys Leu Ser Leu Ser His Asn Cys Ile Ala Gln Ala
 500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Lys Val Leu Asp
 515 520 525

Leu Ser Tyr Asn Lys Leu Asp Leu Tyr His Ser Lys Ser Phe Ser Glu
 530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
 545 550 555 560

Ser Met Gln Gly Ile Gly His Asn Phe Ser Phe Leu Ala Asn Leu Ser
 565 570 575

Arg Leu Gln Asn Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val
 580 585 590

Ser Ser Arg Leu Tyr Ser Thr Ser Val Glu Tyr Leu Asp Phe Ser Gly
 595 600 605

Asn Gly Val Gly Arg Met Trp Asp Glu Glu Asp Leu Tyr Leu Tyr Phe
 610 615 620

Phe Gln Asp Leu Arg Ser Leu Ile His Leu Asp Leu Ser Gln Asn Lys
 625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asn Tyr Leu Pro Lys Ser Leu
 645 650 655

Thr Lys Leu Ser Phe Arg Asp Asn His Leu Ser Phe Phe Asn Trp Ser
 660 665 670

Ser Leu Ala Phe Leu Pro Asn Leu Arg Asp Leu Asp Leu Ala Gly Asn
 675 680 685

Leu Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
 690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Phe Val Val Pro Ala
 705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn

725

730

735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
 740 745 750

Leu Thr Val Leu Asp Val Ser Ser Asn Pro Leu His Cys Ala Cys Gly
 755 760 765

Ala Pro Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly
 770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Arg Gln Leu Gln Gly Arg
 785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Asp Val Leu Ser
 805 810 815

Arg Asp Cys Phe Gly
 820

<210> 3
 <211> 3099
 <212> DNA
 <213> Rattus norvegicus

<400> 3
 atggttctct gtcgcaggac cctgcacccc ttgtctctcc tggtagcaggc cgcagtgtctg 60
 gctgaggctc tggccctggg taccctgcct gccttcctac cctgtgaact gaagcctcat 120
 ggccctggttag actgcaactg gctcttcctg aagtctgtgc ctcaattctc tgccgcagaa 180
 ccccggtcca acatcaccag cctttccttg atcgccaacc gcatccacca cctgcacaac 240
 ctgcactttg tccacctgcc caacgtgcga cagctgaacc tcaagtggaa ctgtccgccc 300
 cctggcctca gccccttgca cttctcctgc cgcattgacca ttgagcccaa aaccttcctg 360
 gctatgctga tgctggaaga gctgaacctg agctataacg gtatcaccac tgtgccccgc 420
 ctgcccagct ccctgacgaa tctgagccta agccacacca acatcctggg actcgatgcc 480
 agcagcctcg ctggcctgca cagcctgcga gttctcttca tggacgggaa ctgctactac 540
 aagaaccctt gcaacggggc ggtgaacgtg acccgggacg ccttcctggg cttgagcaac 600
 ctcacccact tgtcccttaa gtataacaac ctcacagagg tgccccgcca actgcccccc 660
 agcctggagt acctcctgct gtcctataac ctcacgtgca agctgggggc cgaagacctt 720
 gccaacctga cctcccttcg aatgcttgat gtgggtggga attgccgtcg ctgtgatcac 780

gcccccgacc tctgtacaga atgccggcag aagtccttg atctgcaccc tcagactttc	840
catcacctga gccaccttga aggcctggtg ctgaaggaca gttctctcca ctcgctgaac	900
tccaagtggg tccagggctc ggcgaaacctc tcgggtgctgg acctaaagga gaactttctc	960
tacgagagca tcaacaaaac cagcgccctt cagaacctga cccgtctgcg caagctcgac	1020
ctgtccttca attactgcaa gaaggtatcg ttcgcccgc tccacctggc aagttccttc	1080
aagagcctgg tgtcgctgca ggagctgaac atgaacggca tcttcttccg cttactcaac	1140
aagaacacgc tcaggtggct ggctggctc cccaagctcc acacgctgca ccttcaaattg	1200
aatttcatca accaggcgca gctcagcgtc tttagtagct tccgagccct tcgctttgtg	1260
gacctgtcca ataatcgcat cagcgggcct ccaacgctgt ccagagtcgc ccccgaaaag	1320
gcagacgagg cggagaaggg ggttccatgg cctgcaagtc tcaccccagc tctcccagc	1380
actcccgtct caaagaactt catggctcagg tgtaagaacc tcagattcac catggacctg	1440
tctcggaaca accaggtgac tatcaagcca gagatgttcg tcaacctctc ccatctccag	1500
tgtctgagcc tgagccacaa ctgcatcgcg caggctgtca atggctctca gttcctgccc	1560
ctgaccaacc tgaaggtgct ggacctgtcc tataacaagc tggacctgta ccattcgaaa	1620
tcgttcagt agctcccaca gttgcaggcc ctggacctga gctacaacag ccagccattc	1680
agcatgcagg ggataggcca caacttcagt tttctggcca atctgtccag gttacagaac	1740
cttagcctgg cacacaatga cattcacagc cgcgtgtcct cagcctcta cagcacctca	1800
gtggagtatc tggacttcag cggcaacggg gtggggccgca tgtgggacga ggaggacctt	1860
tacctctatt tcttccaaga cctgagaagc ctgattcatc tggacctgtc tcagaataag	1920
ctgcacatcc tccggcccca gaacctcaac tacctcccca agagcctgac gaagctgagt	1980
ttccgtgaca atcacctctc tttctttaac tggagcagtc tggccttcct gcccaatctg	2040
cgagacctgg acctggcagg caatctacta aaggccctga ccaacggcac cctgcctaatt	2100
ggcacgctcc tccagaaact ggatgtcagt agcaacagta tcgtctttgt ggtcccagcc	2160
ttctttgctc tggcggtaga gctaaaagag gtcaacctca gccataacat cctcaagact	2220
gtggatcgct cctggtttgg gccattgtg atgaacctga cggttctaga cgtgagcagc	2280
aacctctgct attgtgctg cgggtgcaccc tttgtagact tactgctgga agtgcagacc	2340
aaggtgcctg gcctggctaa cgggtgtgaag tgtggcagtc cccgccagct gcagggccgc	2400
agcatctttg cgcaagacct gcggctgtgc ctggatgacg tcctttctcg ggactgcttt	2460
ggcctttcac tcctggctgt ggcggtgggc acgggtgttc ctttactgca gcatctctgc	2520
ggctgggacg tctggtactg tttccatctg tgccctggcat ggctacctt gctgacctgt	2580

ggccggcgca gcgccaagc tctcccttat gatgccttcg tgggtgttcga taaggcgag 2640
 agcgcggttg ctgactgggt gtataacgag cttcgagtgc ggctagagga gcggcgcggt 2700
 cgccgagccc tacgcttggt tctggaggac cgagattggc tgccctggcca gacactcttc 2760
 gagaacctct gggcctccat ctatggcagc cgcaagactc tgtttgtgct ggcccacacg 2820
 gacaaggtca gtggcctcct gcgcaccagc ttctgtctgg ctcagcagcg cctgctggag 2880
 gaccgcaagg acgtgggtgtt gttgggtgatc ctgcgccttg atgcccaccg ctcccgtac 2940
 gtgcgactgc gccagcgctt ctgccgccag agtgtgtctt tctggcccca tcagcccaac 3000
 gggcagggca gcttctgggc ccagctgagt acagccctga ctagggacaa ccaccacttc 3060
 tataaccgga acttctgccg gggacctaca gcagaatag 3099

<210> 4
 <211> 2463
 <212> DNA
 <213> Rattus norvegicus

<400> 4
 atggttctct gtcgcaggac cctgcacccc ttgtctctcc tggtagaggc cgcagtgtctg 60
 gctgaggctc tggccctggg taccctgcct gccttcctac cctgtgaact gaagcctcat 120
 ggccctggtag actgcaactg gctcttcctg aagtctgtgc ctcacttctc tgccgcagaa 180
 ccccgttcca acatcaccag cctttccttg atcgccaacc gcatccacca cctgcacaac 240
 ctcgactttg tccacctgcc caacgtgcga cagctgaacc tcaagtggaa ctgtccgccc 300
 cctggcctca gcccttgca cttctcctgc cgcctgacca ttgagcccaa aaccttcctg 360
 gctatgcgca tgctggaaga gctgaacctg agctataacg gtatcaccac tgtgccccgc 420
 ctgcccagct ccctgacgaa tctgagccta agccacacca acatcctggt actcgatgcc 480
 agcagcctcg ctggcctgca cagcctgcga gttctcttca tggacgggaa ctgctactac 540
 aagaaccctt gcaacggggc ggtgaacgtg accccggagc ccttcctggg cttgagcaac 600
 ctcacccact tgtcccttaa gtataacaac ctcacagagg tgccccgcca actgcccccc 660
 agcctggagt acctcctgct gtcctataac ctcacgtca agctgggggc cgaagacctc 720
 gccaacctga cctcccttcg aatgcttgat gtgggtggga attgccgtcg ctgtgatcac 780
 gccccgacc tctgtacaga atgccggcag aagtcccttg atctgcaccc tcagactttc 840
 catcacctga gccaccttga aggcctgggt ctgaaggaca gttctctcca ctcgctgaac 900
 tccaagtggg tccagggctt ggcaaacctc tcgggtgttg acctaaagca gaactttctc 960
 tacgagagca tcaacaaaac cagcgccttt cagaacctga cccgtctgcg caagctcgac 1020

```

ctgtccttca attactgcaa gaaggatatcg ttcccccgc tccacctggc aagttccttc 1080
aagagcctgg tgtcgctgca ggagctgaac atgaacggca tcttcttccg cttactcaac 1140
aagaacacgc tcaggtggct ggctgggtctg cccaagctcc acacgctgca ccttcaaattg 1200
aatattcatca accaggcgca gctcagcgtc tttagtacct tccgagccct tcgctttgtg 1260
gacctgtcca ataatcgcat cagcgggcct ccaacgctgt ccagagtcgc ccccgaaaag 1320
gcagacgagg cggagaaggg ggttccatgg cctgcaagtc tcaccccagc tctcccagac 1380
actcccgctc caaagaactt catgggtcagg tgtaagaacc tcagattcac catggacctg 1440
tctcggaaaca accaggtgac tatcaagcca gagatgttcg tcaacctctc ccattctccag 1500
tgtctgagcc tgagccacaa ctgcatcgcg caggctgtca atggctctca gttcctgccc 1560
ctgaccaacc tgaaggtgct ggacctgtcc tataacaagc tggacctgta ccattcgaaa 1620
tcgttcagtg agctcccaca gttgcaggcc ctggacctga gctacaacag ccagccattc 1680
agcatgcagg ggataggcca caacttcagt tttctggcca atctgtccag gttacagaac 1740
cttagcctgg cacacaatga cattcacagc cgcgtgtcct cagcctcta cagcacctca 1800
gtggagtatc tggacttcag cggcaacggg gtgggcccga tgtgggacga ggaggacctt 1860
tacctctatt tcttccaaga cctgagaagc ctgattcatc tggacctgtc tcagaataag 1920
ctgcacatcc tccggcccca gaacctcaac tacctcccca agagcctgac gaagctgagt 1980
ttccgtgaca atcacctctc tttctttaac tggagcagtc tggccttcct gcccaatctg 2040
cgagacctgg acctggcagg caatctacta aaggccctga ccaacggcac cctgcctaatt 2100
ggcacgctcc tccagaaact ggatgtcagt agcaacagta tcgtctttgt ggtcccagcc 2160
ttctttgctc tggcggtaga gctaaaagag gtcaacctca gccataacat cctcaagact 2220
gtggatcgct cctgggtttg gccattgtg atgaacctga cggttctaga cgtgagcagc 2280
aaccctctgc attgtgcctg cgggtgcacc tttgtagact tactgctgga agtgagacc 2340
aaggtgcctg gcctggctaa cgggtgtgaag tgtggcagtc cccgccagct gcagggccgc 2400
agcatctttg cgcaagacct gcggctgtgc ctggatgacg tcctttctcg ggactgcttt 2460
ggc 2463

```

```

<210> 5
<211> 1030
<212> PRT
<213> Sus scrofa
<400> 5

```

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val
 1 5 10 15
 Thr Ala Leu Ala Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu
 20 25 30
 Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe
 35 40 45
 Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val
 50 55 60
 Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser
 65 70 75 80
 Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn
 85 90 95
 Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr
 100 105 110
 Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
 115 120 125
 Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu
 130 135 140
 Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr
 145 150 155 160
 His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn
 165 170 175
 Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly
 180 185 190
 Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
 195 200 205
 Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu
 210 215 220
 Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro
 260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg
 290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
 305 310 315 320

Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg
 325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
 340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln
 370 375 380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu
 405 410 415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
 420 425 430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro
 435 440 445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp
 450 455 460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg
 465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg
 485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn
 500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser
 515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro
 530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met
 545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu
 565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln
 580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp
 595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln
 610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His
 625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His
 645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu
 660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu
 675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg
 690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe

705		710		715		720
Ala Leu Ala Lys	Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu					
	725			730		735
Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys						
	740			745		750
Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr						
	755			760		765
Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro						
	770			775		780
Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile						
	785			790		795
						800
Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn						
	805			810		815
Cys Phe Gly Ile Ser Leu Leu Ala Met Ala Leu Gly Leu Val Val Pro						
	820			825		830
Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu						
	835			840		845
Cys Leu Ala Trp Leu Pro His Arg Gly Gln Arg Arg Gly Ala Asp Ala						
	850			855		860
Leu Phe Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val						
	865			870		875
						880
Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg						
	885			890		895
Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro						
	900			905		910
Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg						
	915			920		925
Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu						
	930			935		940

Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys
 945 950 955 960

Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala Tyr Arg Ser Arg
 965 970 975

Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp
 980 985 990

Pro His Gln Pro Arg Gly Gln Gly Ser Phe Trp Ala Gln Leu Gly Thr
 995 1000 1005

Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg Asn Phe Cys
 1010 1015 1020

Arg Gly Pro Thr Thr Ala Glu
 1025 1030

<210> 6
 <211> 819
 <212> PRT
 <213> Sus scrofa

<400> 6

Met Gly Pro Arg Cys Thr Leu His Pro Leu Ser Leu Leu Val Gln Val
 1 5 10 15

Thr Ala Leu Ala Ala Ala Leu Ala Gln Gly Arg Leu Pro Ala Phe Leu
 20 25 30

Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu Phe
 35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Ala Asn Val
 50 55 60

Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp Ser
 65 70 75 80

Asp Phe Val His Leu Ser Ser Leu Arg Thr Leu Asn Leu Lys Trp Asn
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met Thr
 100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
 115 120 125

Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Asp Ser Leu
 130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro Thr
 145 150 155 160

His Leu Thr Gly Leu His Ala Leu Arg Tyr Leu Tyr Met Asp Gly Asn
 165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gly Ala Leu Glu Val Val Pro Gly
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
 195 200 205

Asn Leu Thr Glu Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Thr Leu
 210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Thr Pro Glu Asp Leu Ala
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asp His Pro
 260 265 270

Lys Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asp Thr Arg Trp Phe Arg
 290 295 300

Gly Leu Asp Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
 305 310 315 320

Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Arg Leu Arg
 325 330 335

Ser Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
 340 345 350

Leu His Leu Ala Pro Ser Phe Gly His Leu Arg Ser Leu Lys Glu Leu
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu Gln
 370 375 380

Pro Leu Val Gln Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met Asn
 385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly Leu
 405 410 415

Leu Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
 420 425 430

Val Ala Ile Thr Arg Glu Val Asp Gly Arg Glu Arg Val Trp Leu Pro
 435 440 445

Ser Arg Asn Leu Ala Pro Arg Pro Leu Asp Thr Leu Arg Ser Glu Asp
 450 455 460

Phe Met Pro Asn Cys Lys Ala Phe Ser Phe Thr Leu Asp Leu Ser Arg
 465 470 475 480

Asn Asn Leu Val Thr Ile Gln Ser Glu Met Phe Ala Arg Leu Ser Arg
 485 490 495

Leu Glu Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn
 500 505 510

Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser
 515 520 525

His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro
 530 535 540

Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Thr Met
 545 550 555 560

Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala Leu
 565 570 575

Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser Gln
 580 585 590

Gln Leu Cys Ser Ala Ser Leu Cys Ala Leu Asp Phe Ser Gly Asn Asp
 595 600 605

Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe Gln
 610 615 620

Gly Leu Arg Ser Leu Val Trp Leu Asp Leu Ser Gln Asn His Leu His
 625 630 635 640

Thr Leu Leu Pro Arg Ala Leu Asp Asn Leu Pro Lys Ser Leu Lys His
 645 650 655

Leu His Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu
 660 665 670

Thr Leu Leu Pro Lys Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln Leu
 675 680 685

Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Arg Arg
 690 695 700

Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Asn Pro Gly Phe Phe
 705 710 715 720

Ala Leu Ala Lys Gln Leu Glu Glu Leu Asn Leu Ser Ala Asn Ala Leu
 725 730 735

Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Met Val Gly Asn Leu Lys
 740 745 750

Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Thr
 755 760 765

Phe Val Gly Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu Pro
 770 775 780

Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly His Ser Ile
 785 790 795 800

Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Trp Asn
 805 810 815

Cys Phe Gly

<210> 7
 <211> 3352
 <212> DNA
 <213> Sus scrofa

<400> 7
 gagcacgaac atccttcact gtagctgctg cccggtctgc cagccagacc ctttggagaa 60
 gaccccactc cctgtcatgg gccccgctg caccctgcac cccctttctc tcctgggtgca 120
 ggtgacagcg ctgggtgcgg ctctggccca gggcaggctg cctgccttcc tgccctgtga 180
 gctccagccc cacggcctgg tgaactgcaa ctggctcttc ctgaagtccg tgccccactt 240
 ctcggcggca gcgccccggg ccaacgtcac cagcctctcc ttactctcca accgcatcca 300
 ccacctgcac gactccgact tcgtccacct gtccagccta cgaactctca acctcaagtg 360
 gaactgcccc cgggctggcc tcagccccat gcaattcccc tgccacatga ccatcgagcc 420
 caacaccttc ctggcctgct ccaccctgga ggagctgaac ctgagctaca acagcatcac 480
 gaccgtgcct gccctgccc actccctcgt gtccctgtcg ctgagccgca ccaacatcct 540
 ggtgctagac cccaccacc tcaactggcct acatgccctg cgctacctgt acatggatgg 600
 caactgctac tacaagaacc cctgccaggg ggcgctggag gtggtgccgg gtgccctcct 660
 cggcctgggc aacctcacac atctctcact caagtacaac aatctcacgg aggtgccccg 720
 cagcctgccc cccagcctgg agaccctgct gttgtcctac aaccacattg tcaccctgac 780
 gcctgaggac ctggccaatc tgactgccct gcgcgtgctt gatgtggggg ggaactgccg 840
 ccgctgtgac catgcccgca acccctgcag ggagtgcccc aaggaccacc ccaagctgca 900
 ctctgacacc ttcagccacc tgagccgcct cgaaggcctg gtgttgaaag acagttctct 960
 ctacaacctg gacaccaggt ggttcogagg cctggacagg ctccaagtgc tggacctgag 1020
 tgagaacttc ctctacgact gcatcaccaa gaccacggcc ttccagggcc tggccccgact 1080
 gcgcagcctc aacctgtcct tcaattacca caagaagggtg tcctttgccc acctgcacct 1140
 ggcaccctcc tttgggcacc tccggctcct gaaggagctg gacatgcatg gcatcttctt 1200
 ccgctcgctc agtgagacca cgctccaacc tctgggtccaa ctgcctatgc tccagaccct 1260
 gcgcctgcag atgaacttca ttaaccaggc ccagctcagc atctttgggg ccttcctctg 1320
 cctgctgtac gtggacctat cggacaaccg catcagcgga gctgcaaggc cagtggccat 1380
 tactagggag gtggatggta gggagagggt ctggctgcct tccaggaacc tcgctccacg 1440
 tccactggac actctccgct cagaggactt catgccaaac tgcaaggcct tcagcttcac 1500

cttggacctg tctcgggaaca acctggtgac aatccagtcg gagatgtttg ctgcctctc	1560
acgcctcgag tgcctgcgcc tgagccacaa cagcatctcc caggcggtca atggctctca	1620
gtttgtgccg ctgaccagcc tgcgggtgct ggacctgtcc cacaacaagc tggacctgta	1680
tcacggggcg tcgttcacgg agctgccgag cctggaagca ctggacctca gctacaatag	1740
ccagcccttt accatgcagg gtgtgggcca caacctcagc ttctgtggccc agctgcccgc	1800
cctgcgctac ctgagcctgg cgcacaatga catccatagc cgagtgtccc agcagctctg	1860
tagcgctca ctgtgcgcc tggactttag cggcaacgat ctgagccgga tgtgggctga	1920
gggagacctc tatctccgct tcttccaagg cctaagaagc ctagtctggc tggacctgtc	1980
ccagaaccac ctgcacacc tcctgccagc tgccctggac aacctcccca aaagcctgaa	2040
gcatctgcat ctccgtgaca ataacctggc cttcttcaac tggagcagcc tgacctctc	2100
gccaagctg gaaaccttg acttggttg aaaccagctg aaggccctaa gcaatggcag	2160
cctgccatct ggcaccagc tgcggaggct ggacctcagt ggcaacagca tcggctttgt	2220
gaacctggc ttctttgcc tggccaagca gttagaagag ctcaacctca gcgccaatgc	2280
cctcaagaca gtggagccct cctggtttg ctgatggtg ggcaacctga aagtcctaga	2340
cgtgagcgcc aacctctgc actgtgctg tggggcgacc ttctgtggct tcctgctgga	2400
ggtacaggct gccgtgctg ggctgcccag ccgcgtcaag tgtggcagtc cggggcagct	2460
ccagggccat agcatctttg cgcaagacct gcgcctctgc ctggatgaga ccctctctg	2520
gaactgtttt ggcattctgc tgetggccat ggccctgggc ctggttgtgc ccatgctgca	2580
ccacctctgc ggctgggacc tctggtactg cttccacctg tgccctggcct ggctgcccc	2640
ccgagggcag cggcggggag cagacgccct gttctatgat gccttcgtgg tctttgacaa	2700
agctcagagt gctgtggccg actgggtgta caacgagctg cgggtgcagc tggaggagcg	2760
ccgtggggcg cgcgactgc gcctgtgct ggaggagcga gactggttac ctggcaagac	2820
gctcttcgag aacctgtggg cctcagtcta cagcagccgc aagaccctgt ttgtgctggc	2880
ccacacggac cgtgtcagcg gcctcttgag tgccagtttc ctgctggccc agcagcgct	2940
gctggaggac cgcaaggacg ttgtagtgt ggtgatcctg cgcctcgatg cctaccgctc	3000
ccgtacgtg cggctgcgcc agcgctctg ccgccagagt gtcctcctct ggccccacca	3060
gccccgtggg cagggcagct tctgggcca gctgggcaca gccctgacca gggacaacca	3120
ccacttctat aaccggaact tctgccgggg cccacagaca gccgaatagc actgagtgc	3180
agcccgattg cccagcccc cctggatttg cctctctgcc tggggtgccc caacctgctt	3240
tgctcagcca caccactgct ctgctccctg tccccaccc cccccccag cctggcatgt	3300

aacatgtgcc caataaatgc taccggaggg ccaagaaaaa aaaaaaaaaa aa 3352

<210> 8
 <211> 2457
 <212> DNA
 <213> Sus scrofa

<400> 8
 atgggcccc gctgcaccct gcaccccctt totctcctgg tgcaggtgac agcgctggct 60
 gcggctctgg ccagggcag gctgcctgcc ttctgccct gtgagctcca gcccacggc 120
 ctggtgaact gcaactggct cttctgaag tccgtgcccc acttctcggc ggcagcgccc 180
 cgggccaacg tcaccagcct ctccttactc tccaaccgca tccaccacct gcacgactcc 240
 gacttcgtcc acctgtccag cctacgaact ctcaacctca agtggaactg cccgccggct 300
 ggctcagcc ccatgcactt cccctgccac atgaccatcg agcccaacac ctctctggcc 360
 gtgcccaccc tggaggagct gaacctgagc tacaacagca tcacgacogt gcctgccctg 420
 cccgactccc tcgtgtccct gtgcgtgagc cgcaccaaca tcttgggtgt agaccccacc 480
 cacctcactg gcctacatgc cctgcgtac ctgtacatgg atggcaactg ctactacaag 540
 aaccctgcc agggggcgct ggagggtggg ccgggtgccc tctcggcct gggcaacctc 600
 acacatctct cactcaagta caacaatctc acggagggtgc cccgcagcct gccccccagc 660
 ctggagaccc tgctgttgct ctacaaccac attgtcacc tgacgcctga ggacctggcc 720
 aatctgactg ccctgcgcgt gcttgatgtg ggggggaact gccgccgctg tgacctgcc 780
 cgcaaccct gcagggagtg cccaaaggac caccacaagc tgcactctga caccttcagc 840
 cacctgagcc gctcgaagg cctgggtgtg aaagacagtt ctctctacaa cctggacacc 900
 aggtggttcc gaggcctgga caggctccaa gtgctggacc tgagtgagaa ctctctctac 960
 gactgcatca ccaagaccac ggcttccag ggctggccc gactgcgcag cctcaacctg 1020
 tccttcaatt accacaagaa ggtgtccttt gccacctgc acctggcacc ctctttggg 1080
 cacctccggt ccctgaagga gctggacatg catggcatct tcttccgctc gctcagttag 1140
 accacgctcc aacctctggt ccaactgcct atgctccaga ccctgcgcct gcagatgaac 1200
 ttcattaacc aggcccagct cagcatcttt ggggccttcc ctggcctgct gtacgtggac 1260
 ctatcggaca accgcatcag cggagctgca aggccagtgg ccattactag ggaggtggat 1320
 ggtagggaga gggctctggct gccttccagg aacctcgctc cacgtccact ggacactctc 1380
 cgctcagagg acttcatgcc aaactgcaag gccttcagct tcaccttga cctgtctcgg 1440
 aacaacctgg tgacaatcca gtcggagatg tttgtcgcc tctcacgcct cgagtgcctg 1500

cgcttgagcc acaacagcat ctcccaggcg gtcaatggct ctcagtttgt gccgctgacc 1560
 agcctgcggg tgctggacct gtcccacaac aagctggacc tgtatcacgg gcgctcgttc 1620
 acggagctgc cgcgcttggg agcactggac ctcagctaca atagccagcc ctttaccatg 1680
 caggggtgtgg gccacaacct cagcttcgtg gccagctgc ccgccctgcg ctacctcagc 1740
 ctggcgacaca atgacatcca tagccgagtg tcccagcagc tctgtagcgc ctcaactgtgc 1800
 gccctggact ttagcggcaa cgatctgagc cggatgtggg ctgagggaga cctctatctc 1860
 cgcttcttcc aaggcctaag aagcctagtc tggctggacc tgtcccagaa ccacctgcac 1920
 accctcctgc cacgtgccct ggacaacctc cccaaaagcc tgaagcatct gcatctccgt 1980
 gacaataacc tggccttctt caactggagc agcctgacct tcctgcccac gctggaaacc 2040
 ctggacttgg ctggaaacca gctgaaggcc ctaagcaatg gcagcctgcc atctggcacc 2100
 cagctgcgga ggctggacct cagtggcaac agcatcggtt ttgtgaaccc tggcttcttt 2160
 gccctggcca agcagttaga agagctcaac ctcagcgcca atgccctcaa gacagtggag 2220
 ccctcctggt ttggctcgat ggtgggcaac ctgaaagtcc tagacgtgag cgccaaccct 2280
 ctgcactgtg cctgtggggc gaccttcgtg ggcttcctgc tggaggtaca ggctgccgtg 2340
 cctgggctgc ccagccgct caagtgtggc agtccggggc agctccaggg ccatagcatc 2400
 tttgcgcaag acctgcgct ctgcctggat gagacctct cgtggaactg ttttggc 2457

<210> 9

<211> 1029

<212> PRT

<213> Bos taurus

<400> 9

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
 1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu
 20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe
 35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
 50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
 65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro
260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg
290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr

305		310		315		320
Asp Tyr Ile Thr	Lys Thr Thr Ile Phe	Asn Asp Leu Thr	Gln Leu Arg			
	325	330	335			
Arg Leu Asn Leu	Ser Phe Asn Tyr His	Lys Lys Val Ser	Phe Ala His			
	340	345	350			
Leu His Leu Ala	Ser Ser Phe Gly	Ser Leu Val Ser	Leu Glu Lys Leu			
	355	360	365			
Asp Met His Gly	Ile Phe Phe Arg Ser	Leu Thr Asn Ile	Thr Leu Gln			
	370	375	380			
Ser Leu Thr Arg	Leu Pro Lys Leu	Gln Ser Leu His	Leu Gln Leu Asn			
	385	390	395	400		
Phe Ile Asn Gln	Ala Gln Leu Ser	Ile Phe Gly Ala	Phe Pro Ser Leu			
	405	410	415			
Leu Phe Val Asp	Leu Ser Asp Asn	Arg Ile Ser Gly	Ala Ala Thr Pro			
	420	425	430			
Ala Ala Ala Leu	Gly Glu Val Asp	Ser Arg Val Glu	Val Trp Arg Leu			
	435	440	445			
Pro Arg Gly Leu	Ala Pro Gly Pro	Leu Asp Ala Val	Ser Ser Lys Asp			
	450	455	460			
Phe Met Pro Ser	Cys Asn Leu Asn	Phe Thr Leu Asp	Leu Ser Arg Asn			
	465	470	475	480		
Asn Leu Val Thr	Ile Gln Gln Glu	Met Phe Thr Arg	Leu Ser Arg Leu			
	485	490	495			
Gln Cys Leu Arg	Leu Ser His Asn	Ser Ile Ser Gln	Ala Val Asn Gly			
	500	505	510			
Ser Gln Phe Val	Pro Leu Thr Ser	Leu Arg Val Leu	Asp Leu Ser His			
	515	520	525			
Asn Lys Leu Asp	Leu Tyr His Gly	Arg Ser Phe Thr	Glu Leu Pro Gln			
	530	535	540			

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
 545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
 565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
 580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
 595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
 610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr
 625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
 645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
 660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val
 705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
 725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
 755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
 785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
 805 810 815

Phe Gly Leu Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met
 820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys
 835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu
 850 855 860

Leu Tyr Asp Ala Val Val Val Phe Asp Lys Val Gln Ser Ala Val Ala
 865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly
 885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly
 900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys
 915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg
 930 935 940

Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp
 945 950 955 960

Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr
 965 970 975

Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro
 980 985 990

His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Ile Ala
 995 1000 1005

Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg
 1010 1015 1020

Gly Pro Thr Thr Ala Glu
1025

<210> 10
<211> 818
<212> PRT
<213> Bos taurus

<400> 10

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Glu Gly Thr Leu Pro Ala Phe Leu
20 25 30

Pro Cys Glu Leu Gln Pro His Gly Gln Val Asp Cys Asn Trp Leu Phe
35 40 45

Leu Lys Ser Val Pro His Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr
100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu
130 135 140

Val Ser Leu Ser Leu Ser His Thr Ser Ile Leu Val Leu Gly Pro Thr
145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn
165 170 175

Cys Tyr Tyr Met Asn Pro Cys Pro Arg Ala Leu Glu Val Ala Pro Gly
180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu
210 215 220

Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu Ala
225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro
260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg
290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
305 310 315 320

Asp Tyr Ile Thr Lys Thr Thr Ile Phe Asn Asp Leu Thr Gln Leu Arg
325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
340 345 350

Leu His Leu Ala Ser Ser Phe Gly Ser Leu Val Ser Leu Glu Lys Leu
355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Ile Thr Leu Gln
370 375 380

Ser Leu Thr Arg Leu Pro Lys Leu Gln Ser Leu His Leu Gln Leu Asn
385 390 395 400

Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu
405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Thr Pro

420	425	430
Ala Ala Ala Leu Gly Glu Val Asp Ser Arg Val Glu Val Trp Arg Leu		
435	440	445
Pro Arg Gly Leu Ala Pro Gly Pro Leu Asp Ala Val Ser Ser Lys Asp		
450	455	460
Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn		
465	470	475
Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu		
485	490	495
Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly		
500	505	510
Ser Gln Phe Val Pro Leu Thr Ser Leu Arg Val Leu Asp Leu Ser His		
515	520	525
Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln		
530	535	540
Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln		
545	550	555
Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg		
565	570	575
Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys		
580	585	590
Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu		
595	600	605
Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly		
610	615	620
Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Glu Asn His Leu His Thr		
625	630	635
Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu		
645	650	655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
660 665 670

Val Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Ile Arg Leu Gln Lys Leu
690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Ile Pro Gly Phe Phe Val
705 710 715 720

Arg Ala Thr Arg Leu Ile Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
725 730 735

Thr Val Asp Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu Lys Ile
740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
755 760 765

Val Asp Phe Leu Leu Glu Arg Gln Glu Ala Val Pro Gly Leu Ser Arg
770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
785 790 795 800

Thr Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
805 810 815

Phe Gly

<210> 11

<211> 3191

<212> DNA

<213> Bos taurus

<400> 11

```

gggaagtggg cgccaagcat ccttcctgc agctgcctcc caacctgccc gccagacct 60
ctggagaagc cgcattccct gtcattggcc cctactgtgc cccgcacccc ctttctctcc 120
tggtgcaggc ggcggcactg gcagcggccc tggccgaggg caccctgcct gccttctctgc 180
cctgtgagct ccagcccat ggtaggtgg actgcaactg gctgttcctg aagtctgtgc 240
cgcacttttc ggctggagcc ccccgggcca atgtcaccag cctctcctta atctccaacc 300

```

gcatccacca cttgcatgac tctgacttcg tccacctgtc caacctgcgg gtcctcaacc	360
tcaagtggaa ctgcccgcg gccggcctca gcccctatgca cttcccctgc cgtatgacca	420
tcgagcccaa caccttcctg gctgtgcca cctggagga gctgaacctg agctacaacg	480
gcatcacgac cgtgcctgcc ctgccagtt cctcgtgtc cctgtcgtg agccacacca	540
gcatcctggt gctaggcccc acccacttca cgggcctgca cggcctgcgc tttctgtaca	600
tggacggcaa ctgctactac atgaaccct gccgcgggc cctggagggtg gcccaggcg	660
ccctcctcgg cctgggcaac ctcacgcacc tgctcgtcaa gtacaacaac ctcacggagg	720
tgccccgcg cctgcccccc agcctggaca cctgtgtgt gtctacaac cacattgtca	780
ccctggcacc cgaggacctg gccaacctga ctgccctgcg cgtgcttgac gtgggtggga	840
actgccgcg ctgcgacct gcccgcaacc cctgcaggga gtgccccaaag aacttccccca	900
agctgcaccc tgacaccttc agtcacctga gccgcctcga aggcctggtg ttgaaggaca	960
gttctctcta caaactagag aaagattggt tccgcggcct gggcaggctc caagtgtctg	1020
acctgagtga gaacttcctc tatgactaca tcaccaagac caccatcttc aacgacctga	1080
cccagctgcg cagactcaac ctgtccttca attaccacaa gaagggtgtcc ttcgcccacc	1140
tgcacctagc gtctctcttt gggagtctgg tgtccctgga gaagctggac atgcacggca	1200
tcttcttccg ctccctcacc aacatcacgc tccagtcgt gacccggctg cccaagctcc	1260
agagtctgca tctgcagctg aacttcatca accaggccca gctcagcatc tttggggcct	1320
tcccgagcct gctcttcgtg gacctgtcgg acaaccgcat cagcggagcc gcgacgccag	1380
cggccgcctt gggggagggtg gacagcaggg tggaagtctg gcgattgcc aggggcctcg	1440
ctccaggccc gctggacgcc gtcagctcaa aggacttcat gccaagctgc aacctcaact	1500
tcaccttgga cctgtcacgg aacaacctgg tgacaatcca gcaagagatg tttaccgcc	1560
tctccgcct ccagtgcctg cgctgagcc acaacagcat ctgcaggcg gttaatggct	1620
cccagttcgt gccgctgacc agcctgcgag tgctcgacct gtcccacaac aagctggacc	1680
tgtaccatgg gcgctcatc acggagctgc cgcagctgga ggcactggac ctgagctaca	1740
acagccagcc cttcagcatg cagggcgtgg gccacaacct cagcttcgtg gccagctgc	1800
cctccctgcg ctacctcagc cttgcgcaca atggcatcca cagccgcgtg tcacagaagc	1860
tcagcagcgc ctggttgcc gccctggact tcagcggcaa ctccctgagc cagatgtggg	1920
ccgagggaga cctctatctc tgctttttca aaggcttgag gaacctggtc cagctggacc	1980
tgtccgagaa ccatctgcac accctcctgc ctgctcacct ggacaacctg cccaagagcc	2040

tgcggcagct gcgtctccgg gacaataacc tggccttctt caactggagc agcctgaccg 2100
 tcctgccccg gctggaagcc ctggatctgg caggaaacca gctgaaggcc ctgagcaacg 2160
 gcagcctgcc gcctggcatc cggctccaga agctggacgt gagcagcaac agcatcggct 2220
 tcgtgatccc cggcttcttc gtcgcgcga ctcggctgat agagcttaac ctcagcgcca 2280
 atgccctgaa gacagtggat cctccttggg tcggttcctt agcagggacc ctgaaaatcc 2340
 tagacgtgag cgccaacccg ctccactgcg cctgcggggc ggcctttgtg gacttcctgc 2400
 tggagagaca ggaggccgtg cccgggctgt ccaggcgcgt cacatgtggc agtccgggccc 2460
 agctccaggg ccgcagcatc ttcacacagg acctgcgcct ctgcctggat gagaccctct 2520
 ccttggactg ctttggcctc tcaactgctaa tgggtggcgt gggcctggca gtgcccatgc 2580
 tgcaccacct ctgtggctgg gacctctggg actgcttcca cctgtgtctg gcccatctgc 2640
 cccgacggcg gcggcagcgg ggcgaggaca cctgctcta tgatgccgtc gtggtcttcg 2700
 acaaggtgca gagtgcagtg gctgattggg tgtacaacga gctccgcgtg cagctggagg 2760
 agcgccgggg gcgcccggcg ctccgcctct gcctggagga gcgagactgg ctccctggta 2820
 agacgtcttt cgagaacctg tgggcctcgg tctacagcag ccgcaagacc atgttcgtgc 2880
 tggaccacac ggaccgggtc agcggcctcc tgcgcgccag cttcctgctg gccagcagc 2940
 gcctgttggg ggaccgcaag gacgtcgtag tgctggtgat cctgcgcccc gccgcctatc 3000
 ggtcccgtc cgtgcggctg cgccagcgcc tctgcccca gagcgtctc ctctggcccc 3060
 accagcccag tggccagggt agtttctggg ccaacctggg catagccctg accagggaca 3120
 accgtcactt ctataaccgg aacttctgcc ggggccccac gacagccgaa tagcacagag 3180
 tgactgccc g 3191

<210> 12
 <211> 2454
 <212> DNA
 <213> Bos taurus

<400> 12
 atgggcccc actgtgcccc gcacccctt tctctcctgg tgcaggcggc ggcactggca 60
 gcggccctgg ccgagggcac cctgcctgcc ttctgcct gtgagctcca gcccattggt 120
 cagggtggact gcaactggct gttcctgaag tctgtgccgc acttttcggc tggagcccc 180
 cgggccaatg tcaccagcct ctcttaatc tccaaccgca tccaccactt gcatgactct 240
 gacttcgtcc acctgtccaa cctgcgggtc ctcaacctca agtggaaactg cccgccggcc 300
 ggctcagcc ccatgcactt cccctgccgt atgaccatcg agcccaacac cttcctggct 360

gtgcccaccc	tggaggagct	gaacctgagc	tacaacggca	tcacgaccgt	gcctgccctg	420
cccagttccc	tcgtgtccct	gtcgctgagc	cacaccagca	tcctgggtgct	aggccccacc	480
cacttcaccg	gcctgcacgc	cctgcgcttt	ctgtacatgg	acggcaactg	ctactacatg	540
aacccttgcc	cgcgggccct	ggaggtggcc	ccaggcgccc	tcctcggcct	gggcaacctc	600
acgcacctgt	cgctcaagta	caacaacctc	acggaggtgc	cccgcgcct	gccccccagc	660
ctggacaccc	tgctgctgtc	ctacaaccac	attgtcaccc	tggcaccgga	ggacctggcc	720
aacctgactg	ccctgcgcgt	gcttgacgtg	ggtgggaact	gccgcgcgtg	cgaccatgcc	780
cgcaaccctt	gcagggagtg	cccaaagaac	ttccccaaagc	tgcaccctga	caccttcagt	840
cacctgagcc	gcctcgaagg	cctgggtgtt	aaggacagtt	ctctctacaa	actagagaaa	900
gattggttcc	gcggcctggg	caggctccaa	gtgctcgacc	tgagtgagaa	cttcctctat	960
gactacatca	ccaagaccac	catcttcaac	gacctgaccc	agctgcgcag	actcaacctg	1020
tccttcaatt	accacaagaa	ggtgtccttc	gcccacctgc	acctagcgtc	ctcctttggg	1080
agtctggtgt	ccctggagaa	gctggacatg	cacggcatct	tcttccgctc	cctcaccaac	1140
atcacgctcc	agtcgctgac	ccggctgccc	aagctccaga	gtctgcatct	gcagctgaac	1200
ttcatcaacc	aggcccagct	cagcatcttt	ggggccttcc	cgagcctgct	cttcgtggac	1260
ctgtcggaca	accgcatcag	cggagccgcg	acgccagcgg	ccgccctggg	ggaggtggac	1320
agcaggggtg	aagtctggcg	attgcccagg	ggcctcgctc	caggcccgt	ggacgccgtc	1380
agctcaaagg	acttcatgcc	aagctgcaac	ctcaacttca	ccttggacct	gtcacggaac	1440
aacctggtga	caatccagca	agagatgttt	accgcctct	cccgcctcca	gtgcctgcgc	1500
ctgagccaca	acagcatctc	gcaggcggtt	aatggctccc	agttcggtcc	gctgaccagc	1560
ctgcgagtgc	tcgacctgtc	ccacaacaag	ctggacctgt	accatgggcg	ctcattcacg	1620
gagctgccgc	agctggaggc	actggacctc	agctacaaca	gccagccctt	cagcatgcag	1680
ggcgtggggc	acaacctcag	cttcgtggcc	cagctgccct	ccctgcgcta	cctcagcctt	1740
gcgcacaatg	gcatccacag	ccgcgtgtca	cagaagctca	gcagcgcctc	gttgcgcgcc	1800
ctggacttca	gcggcaactc	cctgagccag	atgtgggccc	aggagagacct	ctatctctgc	1860
tttttcaaag	gcttgaggaa	cctggtccag	ctggacctgt	ccgagaacca	tctgcacacc	1920
ctcctgcctc	gtcacctgga	caacctgccc	aagagcctgc	ggcagctgcg	tctccgggac	1980
aataacctgg	ccttcttcaa	ctggagcagc	ctgaccgtcc	tgccccggct	ggaagccctg	2040
gatctggcag	gaaaccagct	gaaggccctg	agcaacggca	gcctgccgcc	tggcatccgg	2100
ctccagaagc	tggacgtgag	cagcaacagc	atcggtctcg	tgatccccgg	cttcttcgtc	2160

cgcgcgactc ggctgataga gcttaacctc agcgccaatg ccctgaagac agtggatccc 2220
 tcctgggttcg gttccttagc agggaccctg aaaatcctag acgtgagcgc caacccgctc 2280
 cactgcgctt gcggggcggc ctttgtggac ttcctgctgg agagacagga ggccgtgccc 2340
 gggctgtcca ggcgcgtcac atgtggcagt ccggggccagc tccagggccg cagcatcttc 2400
 acacaggacc tgcgcctctg cctggatgag accctctcct tggactgctt tggc 2454

<210> 13

<211> 1031

<212> PRT

<213> Equus caballus

<400> 13

Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn
 50 55 60

Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp
 65 70 75 80

Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met
 100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
 130 135 140

Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro
 145 150 155 160

Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe
 260 265 270

Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe
 290 295 300

Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
 340 345 350

His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu
 370 375 380

Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly
 405 410 415

Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu
 420 425 430

Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu
 435 440 445

Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu
 450 455 460

Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser
 465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser
 485 490 495

Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val
 500 505 510

Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
 515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
 530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
 545 550 555 560

Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr
 565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser
 580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn
 595 600 605

Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe
 610 615 620

Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu
 625 630 635 640

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln
 645 650 655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
 660 665 670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln
 675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln
 690 695 700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe
 705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
 725 730 735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu
 740 745 750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
 755 760 765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp
 805 810 815

Asp Cys Phe Gly Leu Ser Leu Leu Val Val Ala Leu Gly Leu Ala Met
 820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His
 835 840 845

Leu Gly Leu Ala Trp Leu Pro Arg Arg Gly Trp Gln Arg Gly Ala Asp
 850 855 860

Ala Leu Ser Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala

865 870 875 880
 Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg
 885 890 895
 Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu
 900 905 910
 Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser
 915 920 925
 Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Gln Val Ser Gly Leu
 930 935 940
 Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg
 945 950 955 960
 Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Ala Arg Arg Ser
 965 970 975
 Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Phe
 980 985 990
 Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly
 995 1000 1005
 Met Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln Asn Phe
 1010 1015 1020
 Cys Arg Gly Pro Thr Met Ala Glu
 1025 1030

 <210> 14
 <211> 820
 <212> PRT
 <213> Equus caballus

 <400> 14
 Met Gly Pro Cys His Gly Ala Leu Gln Pro Leu Ser Leu Leu Val Gln
 1 5 10 15
 Ala Ala Met Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Pro Phe
 20 25 30
 Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu

35

40

45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Asp Asn
 50 55 60

Val Thr Ser Leu Ser Leu Leu Ser Asn Arg Ile His His Leu His Asp
 65 70 75 80

Ser Asp Phe Ala Gln Leu Ser Asn Leu Gln Lys Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys His Met
 100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
 130 135 140

Leu Val Ser Leu Ile Leu Ser Arg Thr Asn Ile Leu Gln Leu Asp Pro
 145 150 155 160

Thr Ser Leu Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gly Arg Ala Leu Glu Val Ala Pro
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Thr Val Pro Arg Ser Leu Pro Pro Ser Leu Glu Tyr
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Val Thr Leu Ala Pro Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Val Glu Cys Pro His Lys Phe
 260 265 270

Pro Gln Leu His Ser Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Gln Leu Asn Pro Arg Trp Phe
 290 295 300

Arg Gly Leu Gly Asn Leu Thr Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Ala Gln Leu
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
 340 345 350

His Leu Thr Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Gln Lys Thr Leu
 370 375 380

Gln Pro Leu Ala Arg Leu Pro Met Leu Gln Arg Leu Tyr Leu Gln Met
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Lys Asp Phe Pro Gly
 405 410 415

Leu Arg Tyr Ile Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Val Glu
 420 425 430

Pro Val Ala Thr Thr Gly Glu Val Asp Gly Gly Lys Lys Val Trp Leu
 435 440 445

Thr Ser Arg Asp Leu Thr Pro Gly Pro Leu Asp Thr Pro Ser Ser Glu
 450 455 460

Asp Phe Met Pro Ser Cys Lys Asn Leu Ser Phe Thr Leu Asp Leu Ser
 465 470 475 480

Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser
 485 490 495

Arg Leu Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val
 500 505 510

Asn Gly Ser Gln Phe Val Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
 515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
 530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
 545 550 555 560

Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Thr
 565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser
 580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Trp Ala Leu Asp Phe Ser Gly Asn
 595 600 605

Ser Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg Phe Phe
 610 615 620

Gln Gly Leu Arg Ser Leu Ile Arg Leu Asp Leu Ser Gln Asn Arg Leu
 625 630 635 640

His Thr Leu Leu Pro Cys Thr Leu Gly Asn Leu Pro Lys Ser Leu Gln
 645 650 655

Leu Leu Arg Leu Arg Asn Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
 660 665 670

Leu Thr Leu Leu Pro Asn Leu Glu Thr Leu Asp Leu Ala Gly Asn Gln
 675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Ser Gly Thr Gln Leu Gln
 690 695 700

Arg Leu Asp Val Ser Arg Asn Ser Ile Ile Phe Val Val Pro Gly Phe
 705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
 725 730 735

Leu Arg Thr Glu Glu Pro Ser Trp Phe Gly Phe Leu Ala Gly Ser Leu
 740 745 750

Glu Val Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
 755 760 765

Ala Phe Val Asp Phe Leu Leu Gln Val Gln Ala Ala Val Pro Gly Leu
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Lys Ser Leu Ser Trp
 805 810 815

Asp Cys Phe Gly
 820

<210> 15
 <211> 3391
 <212> DNA
 <213> Equus caballus

<400> 15
 ctctgttctc tgagctgttg ccgctgaag ggactgcgag cacaaagcat cctcctctgc 60
 agctgctgcc cagtgtgcca gctggaccct ctggatcatc tccactccc tgtcatgggc 120
 ccttgccatg gtgccctgca gccctgtct ctctgggtgc aggcggccat gctggccgtg 180
 gctctggccc aaggcaccct gcctcccttc ctgccctgtg agctccagcc ccacggcctg 240
 gtgaactgca actggctgtt cctgaagtcc gtgccccact tctcagcagc agcaccgccg 300
 gacaatgtca ccagcctttc cttgctctcc aaccgcatcc accacctcca cgactccgac 360
 ttgcccac tgtccaacct gcagaaactc aacctcaaat ggaactgccc gccagccggc 420
 ctgagcccca tgcacttccc ctgccacatg accatcgagc ccaacacttt cctggctgta 480
 cccaccctgg aggagctgaa cctgagctac aacggcatca cgactgtgcc tgccctgccc 540
 agtccctcg tgccctgat cctgagccgc accaacatcc tgcagctaga cccaccagc 600
 ctacggggc tgcattccct gcgttctcta tacatggatg gcaactgcta ctacaagaac 660
 ccctgcgggc gggccctgga ggtggcccca ggcgccctcc ttggcctggg caacctcacc 720
 cacctgtcac tcaagtacaa caacctcaca acggtgcccc gcagcctgcc ccctagcctg 780
 gactacctgc tgttgtctta caaccacatt gtcaccctgg cacctgagga cctggccaat 840
 ctgactgcc tgcgtgtgct cgatgtgggt ggaaactgcc gccgctgtga ccatgcacgc 900
 aaccctgcg tggagtgcc acataaatc cccagctgc actccgacac cttcagccac 960

ctaagccgcc tagaaggcct cgtgttgaag gatagttctc tctaccagct gaaccccaga	1020
tggttccgtg gcctgggcaa cctcacagtg ctcgacctga gtgagaactt cctctacgac	1080
tgcattacca aaaccaaggc attccagggc ctggcccagc tgogaagact caacttgtcc	1140
ttcaattacc ataagaaggt gtccttcgcc cacctgacgc tggcaccctc cttcgggagc	1200
ctgctctccc tgcaggaact ggacatgcat ggcattctct tccgctcact cagccagaag	1260
acgctccagc cactggcccc cctgcccatt ctccagcgtc tgtatctgca gatgaacttc	1320
atcaaccagg ccagctcgg catcttcaag gacttccctg gtctgcgcta catagacctg	1380
tcagacaacc gcatcagtgg agctgtggag ccggtggcca ccacagggga ggtggatggt	1440
gggaagaagg tctggctgac atccaggac ctactccag gccactgga cccccagc	1500
tctgaggact tcatgccaa ctgcaagaac ctacgcttca ccttggacct gtcacggaac	1560
aacctggtaa cagtccagcc agagatgttt gccagctct cgcgctcca gtgctgcgc	1620
ctgagccaca acagcatctc gcaggcggtc aatggctcac agttcgtgcc actgaccagc	1680
ctgcaggtgc tggacctgtc ccataacaaa ctggacctgt accatgggcg ctcgtttacg	1740
gagctgccgc gactggaggc cctggacctc agctacaaca gccagccctt cagcatgcgg	1800
ggtgtgggcc acaacctcag ctttgtggcc cagctgcca cctgcgcta cctcagcctg	1860
gcacacaatg gcatccacag ccgtgtgtcc cagcagctct gcagcacctc gctgtgggcc	1920
ctggacttca gcggcaattc cctgagccag atgtgggctg agggagacct ctatctccgc	1980
ttcttccaag gcctgagaag cctaattccg ctagacctgt ccagaaatcg tctgcatacc	2040
ctcctgccat gcacctggg caacctcccc aagagcttgc agctgctgcg tctccgtaac	2100
aattacctgg ccttcttcaa ttggagcagc ctgacctcc tgcccaacct ggaaacctg	2160
gacctggctg gaaaccagct gaaggctctg agcaatggca gcctgccttc tggcaccag	2220
ctccagaggc tggacgtcag caggaacagc atcatcttcg tggctccctg cttctttgct	2280
ctggccacga ggctgcgaga gctcaacctc agtgccaacg ccctcaggac agaggagccc	2340
tcctggtttg gtttcttagc aggtccctt gaagtccctag atgtgagcg caacctctg	2400
cactgcgcct gtggggcagc ctttgtggac ttctgctgc aggttcaggc tgccgtgcct	2460
ggtctgcca gccgcgtcaa gtgtggcagt ccgggccagc tccagggccg cagcatcttc	2520
gcacaagacc tgcgcctctg cctggacaag tccctctcct gggactgttt tggctctctca	2580
ttgctggttg tggccctggg cctggccatt cctatgttgc accacctctg cggctgggac	2640
ctctggtact gcttccacct gggcctggcc tggtgcccc ggcgggggtg gcagcggggc	2700

gcggatgccc tgagctatga tgcctttgtg gtcttcgaca aggcacagag cgcagtggcc 2760
 gactgggtgt acaatgaact gcgggtgcgg ctagaggagc gccgtgggag cggggcgctc 2820
 cgcctgtgtc tggaggagcg tgactggcta cctggcaaga cgctgttcga aaacctgtgg 2880
 gcctcagtct acagcagccg caagatgctg tttgtgctgg ccacacgga ccaggtcagt 2940
 ggctctttgc gtgccagctt cctgctggcc cagcagcgctc tgctggagga ccgcaaggac 3000
 gttgtggtgc tggtaatcct gagccctgac gcccgccgtt cccgttacgt gcggctgcgc 3060
 cagcgcctct gccgccagag tgtcctcttc tggccccacc agcctagtgg ccagcgcagc 3120
 ttctgggccc agctaggcat ggccctgacc agggacaacc gccacttcta taaccagaac 3180
 ttctgcccgg gcccgacgat ggctgagtag cacagagtga cagcctggca tgtacaaccc 3240
 ccagccctga ccttgccctc ctgcctatga tgcccagtct gcctcactct gtgacgcccc 3300
 tgctctgcct ccgccaccct caccctggc atacagcagg cactcaataa atgccactgg 3360
 caggccaaac agccaaaaaa aaaaaaaaaa a 3391

<210> 16
 <211> 2460
 <212> DNA
 <213> Equus caballus

<400> 16
 atggggccctt gccatggtgc cctgcagccc ctgtctctcc tgggtgcaggc ggccatgctg 60
 gccgtggctc tggcccaagg caccctgcct cccttctctc cctgtgagct ccagccccac 120
 ggcttggtga actgcaactg gctgttctct aagtccgtgc ccacttctc agcagcagca 180
 ccccgggaca atgtcaccag cctttccttg ctctccaacc gcatccacca cctccacgac 240
 tccgactttg cccaactgtc caacctgcag aaactcaacc tcaaattggaa ctgcccggca 300
 gccggcctca gcccctgca ctccccctgc cacatgacca tcgagcccaa cactttctctg 360
 gctgtacca ccttgagga gctgaacctg agctacaacg gcatcacgac tgtgcctgcc 420
 ctgcccagct cctcgtgtc cctgatcctg agccgcacca acatcctgca gctagacccc 480
 accagcctca cgggcctgca tgccctgcgc ttctataca tggatggcaa ctgctactac 540
 aagaacccct gcgggcgggc cctggaggtg gcccaggcg cctccttgg cctgggcaac 600
 ctcaccacc tgctactcaa gtacaacaac ctcaaacgg tgccccgcag cctgccccct 660
 agcctggagt acctgctgtt gtctacaac cacattgtca cctggcacc tgaggacctg 720
 gccaatctga ctgccctgcg tgtgctcgat gtgggtggaa actgccgccg ctgtgaccat 780
 gcacgcaacc cctgcgtgga tgcccacat aaattcccc agctgcactc cgacaccttc 840

agccacctaa gccgcctaga aggcctcgtg ttgaaggata gttctctcta ccagctgaac 900
 cccagatggt tccgtggcct gggcaacctc acagtgtcgc acctgagtga gaacttcctc 960
 tacgactgca tcacaaaaac caaggcattc cagggcctgg cccagctgcg aagactcaac 1020
 ttgtccttca attaccataa gaagggtgtc ttgcgccacc tgacgctggc accctccttc 1080
 gggagcctgc tctccctgca ggaactggac atgcatggca tcttcttccg ctactcagc 1140
 cagaagacgc tccagccact ggcccgcctg cccatgtctc agcgtctgta tctgcagatg 1200
 aacttcatca accaggccca gctcggcatc ttcaaggact tccctgggtc gcgctacata 1260
 gacctgtcag acaaccgcat cagtggagct gtggagccgg tggccaccac aggggaggtg 1320
 gatggtggga agaaggctctg gctgacatcc agggacctca ctccaggccc actggacacc 1380
 cccagctctg aggacttcat gccaaagtgc aagaacctca gcttcacctt ggacctgtca 1440
 cggaacaacc tggtaacagt ccagccagag atgtttgccc agctctcgcg cctccagtgc 1500
 ctgcgcctga gccacaacag catctcgcag gcggtcaatg gctcacagtt cgtgccactg 1560
 accagcctgc aggtgctgga cctgtcccat aacaaactgg acctgtacca tgggcgctcg 1620
 ttacaggagc tgccgcgact ggaggccctg gacctcagct acaacagcca gcccttcagc 1680
 atgccccgtg tgggccacaa cctcagcttt gtggcccagc tgcccaccct gcgctacctc 1740
 agcctggcac acaatggcat ccacagccgt gtgtcccagc agctctgcag cacctcgtg 1800
 tgggccctgg acttcagcgg caattccctg agccagatgt gggctgaggg agacctctat 1860
 ctccgcttct tccaaggcct gagaagccta atccggctag acctgtccca gaatcgctg 1920
 cataccctcc tgccatgcac cctgggcaac ctccccaaga gcttgagct gctgcgtctc 1980
 cgtaacaatt acctggcctt cttcaattgg agcagcctga ccctcctgcc caacctggaa 2040
 acctggacc tggctggaaa ccagctgaag gctctgagca atggcagcct gccttctggc 2100
 acccagctcc agaggctgga cgtcagcagg aacagcatca tcttcgtggg ccctggcttc 2160
 tttgctctgg ccacgaggct gcgagagctc aacctcagt ccaacgccct caggacagag 2220
 gagccctcct gggttggtt cctagcaggc tcccttgaag tcctagatgt gagcgccaac 2280
 cctctgcact gcgcctgtgg ggcagcctt gtggacttcc tgctgcaggt tcaggctgcc 2340
 gtgcctggtc tgcccagccg cgtcaagtgt ggcagtccg gccagctcca gggccgcagc 2400
 atcttcgcac aagacctgcg cctctgcctg gacaagtccc tctcctggga ctgttttggg 2460

<210> 17
 <211> 1029
 <212> PRT
 <213> Ovis aries

<400> 17

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
 1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu
 20 25 30

Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe
 35 40 45

Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
 50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
 65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr
 100 105 110

Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn
 115 120 125

Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu
 130 135 140

Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr
 145 150 155 160

His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn
 165 170 175

Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly
 180 185 190

Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn
 195 200 205

Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu
 210 215 220

Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala
 225 230 235 240

Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg
 245 250 255

Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro
 260 265 270

Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu
 275 280 285

Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg
 290 295 300

Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr
 305 310 315 320

Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg
 325 330 335

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
 340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg
 370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn
 385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
 420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp
 435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp
 450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn
 465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu
 485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly
 500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr
 515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln
 530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
 545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
 565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
 580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
 595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
 610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr
 625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
 645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
 660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val
705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile
740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg
770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
805 810 815

Phe Gly Phe Ser Leu Leu Met Val Ala Leu Gly Leu Ala Val Pro Met
820 825 830

Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His Leu Cys
835 840 845

Leu Ala His Leu Pro Arg Arg Arg Arg Gln Arg Gly Glu Asp Thr Leu
850 855 860

Leu Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val Ala
865 870 875 880

Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu Glu Arg Arg Gly
885 890 895

Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly
900 905 910

Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser Arg Lys
915 920 925

Thr Met Phe Val Leu Asp His Thr Asp Arg Val Ser Gly Leu Leu Arg

930

935

940

Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp
 945 950 955 960

Val Val Val Leu Val Ile Leu Arg Pro Ala Ala Tyr Arg Ser Arg Tyr
 965 970 975

Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro
 980 985 990

His Gln Pro Ser Gly Gln Gly Ser Phe Trp Ala Asn Leu Gly Met Ala
 995 1000 1005

Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Arg Asn Phe Cys Arg
 1010 1015 1020

Gly Pro Thr Thr Ala Glu
 1025

<210> 18
 <211> 818
 <212> PRT
 <213> Ovis aries

<400> 18

Met Gly Pro Tyr Cys Ala Pro His Pro Leu Ser Leu Leu Val Gln Ala
 1 5 10 15

Ala Ala Leu Ala Ala Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe Leu
 20 25 30

Pro Cys Glu Leu Gln Pro Arg Gly Lys Val Asn Cys Asn Trp Leu Phe
 35 40 45

Leu Lys Ser Val Pro Arg Phe Ser Ala Gly Ala Pro Arg Ala Asn Val
 50 55 60

Thr Ser Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asp Ser
 65 70 75 80

Asp Phe Val His Leu Ser Asn Leu Arg Val Leu Asn Leu Lys Trp Asn
 85 90 95

Cys Pro Pro Ala Gly Leu Ser Pro Met His Phe Pro Cys Arg Met Thr

100	105	110
Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu Asn 115 120 125		
Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Ala Leu Pro Ser Ser Leu 130 135 140		
Val Ser Leu Ser Leu Ser Arg Thr Ser Ile Leu Val Leu Gly Pro Thr 145 150 155 160		
His Phe Thr Gly Leu His Ala Leu Arg Phe Leu Tyr Met Asp Gly Asn 165 170 175		
Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Val Glu Val Ala Pro Gly 180 185 190		
Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr Asn 195 200 205		
Asn Leu Thr Glu Val Pro Arg Arg Leu Pro Pro Ser Leu Asp Thr Leu 210 215 220		
Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu Ala 225 230 235 240		
Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg 245 250 255		
Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Asn Phe Pro 260 265 270		
Lys Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu 275 280 285		
Val Leu Lys Asp Ser Ser Leu Tyr Lys Leu Glu Lys Asp Trp Phe Arg 290 295 300		
Gly Leu Gly Arg Leu Gln Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr 305 310 315 320		
Asp Tyr Ile Thr Lys Thr Thr Ile Phe Arg Asn Leu Thr Gln Leu Arg 325 330 335		

Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala His
 340 345 350

Leu Gln Leu Ala Pro Ser Phe Gly Gly Leu Val Ser Leu Glu Lys Leu
 355 360 365

Asp Met His Gly Ile Phe Phe Arg Ser Leu Thr Asn Thr Thr Leu Arg
 370 375 380

Pro Leu Thr Gln Leu Pro Lys Leu Gln Ser Leu Ser Leu Gln Leu Asn
 385 390 395 400

Phe Ile Asn Gln Ala Glu Leu Ser Ile Phe Gly Ala Phe Pro Ser Leu
 405 410 415

Leu Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Arg Pro
 420 425 430

Val Ala Ala Leu Gly Glu Val Asp Ser Gly Val Glu Val Trp Arg Trp
 435 440 445

Pro Arg Gly Leu Ala Pro Gly Pro Leu Ala Ala Val Ser Ala Lys Asp
 450 455 460

Phe Met Pro Ser Cys Asn Leu Asn Phe Thr Leu Asp Leu Ser Arg Asn
 465 470 475 480

Asn Leu Val Thr Ile Gln Gln Glu Met Phe Thr Arg Leu Ser Arg Leu
 485 490 495

Gln Cys Leu Arg Leu Ser His Asn Ser Ile Ser Gln Ala Val Asn Gly
 500 505 510

Ser Gln Phe Val Pro Leu Thr Arg Leu Arg Val Leu Asp Leu Ser Tyr
 515 520 525

Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu Pro Gln
 530 535 540

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Gln
 545 550 555 560

Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ser Leu Arg
 565 570 575

Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg Val Ser Gln Lys
 580 585 590

Leu Ser Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn Ser Leu
 595 600 605

Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Cys Phe Phe Lys Gly
 610 615 620

Leu Arg Asn Leu Val Gln Leu Asp Leu Ser Lys Asn His Leu His Thr
 625 630 635 640

Leu Leu Pro Arg His Leu Asp Asn Leu Pro Lys Ser Leu Arg Gln Leu
 645 650 655

Arg Leu Arg Asp Asn Asn Leu Ala Phe Phe Asn Trp Ser Ser Leu Thr
 660 665 670

Val Leu Pro Gln Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln Leu Lys
 675 680 685

Ala Leu Ser Asn Gly Ser Leu Pro Pro Gly Thr Arg Leu Gln Lys Leu
 690 695 700

Asp Val Ser Ser Asn Ser Ile Gly Phe Val Thr Pro Gly Phe Phe Val
 705 710 715 720

Leu Ala Asn Arg Leu Lys Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
 725 730 735

Thr Val Asp Pro Phe Trp Phe Gly Arg Leu Thr Glu Thr Leu Asn Ile
 740 745 750

Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
 755 760 765

Val Asp Phe Leu Leu Glu Met Gln Ala Ala Val Pro Gly Leu Ser Arg
 770 775 780

Arg Val Thr Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
 785 790 795 800

Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Thr Leu Ser Leu Asp Cys
 805 810 815

Phe Gly

<210> 19
 <211> 3199
 <212> DNA
 <213> Ovis aries

<400> 19
 gtcggcacgg gaagtgagcg ccaagcatcc ttccctgcag ctgccgcca acttgcccgc 60
 cagaccctct ggagaagccg cattccctgc catgggcccc tactgtgccc cgcaccccct 120
 ttctctcctg gtgcaggcgg cggcgctggc agcagccctg gccagggca cctgcctgc 180
 cttcctgccc tgtgagctcc agccccgggg taaggatgaac tgcaactggc tgttcctgaa 240
 gtctgtgccc cgcttttcgg cgggagcccc ccgggccaat gtcaccagcc tctccttaat 300
 ctccaaccgc atccaccact tgcacgactc tgacttcgtc cacctgtcca acctgcccgt 360
 cctcaacctc aagtggaaact gcccgcggc cggcctcagc cccatgcact tcccctgccc 420
 catgaccatc gagcccaaca ccttcctggc tgtgcccacc ctggaggagc tgaacctgag 480
 ctacaatggc atcacgaccg tgcctgccct gccagttct ctcgatatcc tgcgctgag 540
 ccgcaccagc atcctgggtg taggccccac ccacttcacc ggctgcacg cctgcgctt 600
 tctgtacatg gacggcaact gctactataa gaaccctgc cagcaggccg tggagggtggc 660
 cccaggcgcc ctccctggcc tgggcaacct cacgcacctg tcgctcaagt acaacaacct 720
 cacggaggtg ccccgccgcc tgcacccag cctggacacc ctgctgctgt cctacaacca 780
 catcatcacc ctggcaccgc aggacctggc caatctgact gccctgcgtg tgcttgatgt 840
 gggcggggaa tgccgcgct ggcaccacgc ccgcaacccc tgcaggaggt gcccaaagaa 900
 cttccccaag ctgcaccctg acaccttcag ccacctgagc cgctcgaag gcctggtgtt 960
 gaaggacagt tctctctaca aactagagaa agactgggtc cgcggcctgg gcaggctcca 1020
 agtgctcgac ctgagtgaga acttcctcta tgactacatc accaagacca ccatcttcag 1080
 gaacctgacc cagctgcgca gactcaacct gtccttcaat taccacaaga aggtgtcctt 1140
 cgccacctg caactggcac cctcctttgg gggcctgggtg tccttgagaa agctggacat 1200
 gcacggcatc ttcttcgct ccctcaccaa caccacgctc cggccgctga cccagctgcc 1260
 caagctccag agtctgagtc tgcagctgaa cttcatcaac caggccgagc tcagcatctt 1320
 tggggccttc ccgagcctgc tcttcgtgga cctgtcggac aaccgcatca gcggagctgc 1380
 gaggccggtg gccgcctcg gggaggtgga cagcggggtg gaagtctggc ggtggcccag 1440

gggcctcgct ccaggccgc tggccgccgt cagcgcaaag gacttcatgc caagctgcaa	1500
cctcaacttc accttggaac tgtcacggaa caacctgggtg acgatccagc aggagatgtt	1560
taccgcctc tcccgccctc agtgccctgc cctgagccac aacagcatct cgcaggcggt	1620
taatggctcg cagttcgtgc cgctgacctg cctgcgagtg ctcgacctgt cctacaacaa	1680
gctggacctg taccatgggc gctcggtcac ggagctgccg cagctggagg cactggacct	1740
cagctacaac agccagccct tcagcatgca gggcgtgggc cacaacctca gcttcgtggc	1800
ccagctgccg tccctgcgt acctcagcct tgcgcacaac ggcatccaca gccgcgtgtc	1860
acagaagctc agcagcgccct cgctgcgcgc cctggacttc agcggcaact ccctgagcca	1920
gatgtgggccc gagggagacc tctatctctg cttcttcaaa ggcttgagga acctggtcca	1980
gctggacctg tccaagaacc acctgcacac cctcctgcct cgtcacctgg ataacctgcc	2040
caagagcctg cggcagctgc gtctccggga caataacctg gccttcttca actggagcag	2100
cctgactgtt ctgccccagc tggaagccct ggatctggcg ggaaaccagc tgaaggccct	2160
gagcaacggc agcctgccac ctggcaccgc gctccagaag ctggacgtga gcagcaacag	2220
catcggcttt gtgacctctg gcttctttgt ccttgccaac cggctgaaag agcttaacct	2280
cagcgccaac gccctgaaga cagtggatcc cttctgggtc ggctgcttaa cagagacct	2340
gaatatacta gacgtgagcg ccaaccgcct ccactgtgcc tgcggggcgg cctttgtgga	2400
cttctgctg gagatgcagg cggccgtgcc tgggctgtcc aggcgcgtca cgtgtggcag	2460
tccggggccag ctccagggcc gcagcatctt cgcacaggac ctgcgcctct gcctggatga	2520
gacctctctc ttggactgct ttggcttctc gctgctaata gtggcgctgg gcctggcggt	2580
gcccatgctg caccacctct gtggctggga cctgtggtac tgcttccacc tgtgtctggc	2640
ccatttgccc cgacggcggc ggcagcgggg cgaggacacc ctgctctacg atgccttcgt	2700
ggtcttcgac aaggcgcaga gtgcagtggc cgaactgggtg tacaacgagc tccgcgtgca	2760
gctggaggag cgcgcgggc gccgggcgt cgcctctgc ctggaggagc gagactggct	2820
ccctggcaag acgctcttcg agaacctgtg ggcctcggtc tacagcagcc gtaagaccat	2880
gttcgtgctg gaccacacgg accgggtcag tggcctcctg cgcgccagct tctgctggc	2940
ccagcagcgc ctgttgagg accgcaagga tgtcgtgggt ctggtgatcc tgcgccccgc	3000
cgcctaccgg tcccgctacg tgcggctgcg ccagcgcctc tgccgccaga gcgtcctcct	3060
ctggccccac cagcccagtg gccagggtag cttctggggc aacctgggca tggccctgac	3120
cagggacaac cgccacttct ataaccggaa cttctgccgg ggccccacga cagccgaata	3180

gcacagagtg actgcccag

3199

<210> 20

<211> 2454

<212> DNA

<213> Ovis aries

<400> 20

atgggcccct actgtgcccc gcacccccctt tctctcctgg tgcaggcggc ggcgctggca	60
gcagccctgg cccagggcac cctgcctgcc ttcttgccct gtgagctcca gccccggggt	120
aaggtgaact gcaactggct gttcctgaag tctgtgccgc gcttttcggc cggagccccc	180
cgggccaatg tcaccagcct ctccctaatc tccaaccgca tccaccactt gcacgactct	240
gacttcgtcc acctgtccaa cctgcggggtc ctcaacctca agtggaactg cccgccggcc	300
ggcctcagcc ccatgcactt cccctgccgc atgaccatcg agcccaacac ctctctggct	360
gtgcccaccc tggaggagct gaacctgagc tacaatggca tcacgaccgt gcctgcccctg	420
cccagttctc tcgtatccct gtcgctgagc cgcaccagca tcctgggtgt agggcccacc	480
cacttcaccg gcctgcacgc cctgcgcttt ctgtacatgg acggcaactg ctactataag	540
aaacctgccc agcaggccgt ggaggtggcc ccaggcgccc tccttggcct gggcaacctc	600
acgcacctgt cgctcaagta caacaacctc acggaggtgc cccgccgcct gccccccagc	660
ctggacaccc tgctgctgtc ctacaaccac atcatcacc tggcaccgga ggacctggcc	720
aatctgactg ccctgcgtgt gcttgatgtg ggcgggaact gccgccgctg cgaccacgcc	780
cgcaacctct gcagggagtg cccaaagaac ttccccaagc tgcacctga caccttcagc	840
cacctgagcc gcctcgaagg cctgggtgtg aaggacagtt ctctctacaa actagagaaa	900
gactgggttc gcggcctggg caggctccaa gtgctcgacc tgagtgagaa ctctctctat	960
gactacatca ccaagaccac catcttcagg aacctgacct agctgcgcag actcaacctg	1020
tccttcaatt accacaagaa ggtgtccttc gccacctgc aactggcacc ctcttttggg	1080
ggcctgggtg ccctggagaa gctggacatg cacggcatct tcttccgctc cctcaccaac	1140
accacgctcc ggccgctgac ccagctgccc aagctccaga gtctgagtct gcagctgaac	1200
ttcatcaacc aggccgagct cagcatcttt ggggccttcc cgagcctgct ctctgtggac	1260
ctgtcggaca accgcatcag cggagctgcg aggccgggtg ccgccctcgg ggaggtggac	1320
agcgggggtg aagtctggcg gtggcccagg ggcctcgctc caggcccgtt ggccgccgtc	1380
agcgcaaagg acttcatgcc aagctgcaac ctcaacttca ccttggacct gtcacggaac	1440
aacctgggtg cgatccagca ggagatgttt acccgctctt cccgcctcca gtgcctgcgc	1500

```

ctgagccaca acagcatctc gcaggcggtt aatggctcgc agttcgtgcc gctgaccgcg 1560
ctgcgagtgc tcgacctgtc ctacaacaag ctggacctgt accatgggcg ctcgttcacg 1620
gagctgccgc agctggagggc actggacctc agctacaaca gccagccctt cagcatgcag 1680
ggcgtggggc acaacctcag cttcgtggcc cagctgccgt ccctgcgcta cctcagcctt 1740
gcgcacaaag gcatccacag ccgctgtgtc cagaagctca gcagcgctc gctgcgcgcc 1800
ctggacttca gcggcaactc cctgagccag atgtggggcg agggagacct ctatctctgc 1860
ttcttcaaag gcttgaggaa cctgggtccag ctggacctgt ccaagaacca cctgcacacc 1920
ctcctgcctc gtcacctgga taacctgccc aagagcctgc ggcagctgcg tctccgggac 1980
aataacctgg ccttcttcaa ctggagcagc ctgactgttc tgccccagct ggaagccctg 2040
gatctggcgg gaaaccagct gaaggccctg agcaacggca gcctgccacc tggcaccgcg 2100
ctccagaagc tggacgtgag cagcaacagc atcggctttg tgacccttg cttctttgtc 2160
cttgccaacc ggctgaaaga gcttaacctc agcgccaacg ccctgaagac agtggatccc 2220
ttctggttcg gtcgcttaac agagaccctg aatatactag acgtgagcgc caaccgcctc 2280
cactgtgcct gcggggcggc ctttgtggac ttcctgctgg agatgcaggc ggccgtgcct 2340
gggctgtcca ggcgcgtcac gtgtggcagt ccgggccagc tccagggccg cagcatcttc 2400
gcacaggacc tgcgcctctg cctggatgag accctctcct tggactgctt tggc 2454

```

<210> 21
 <211> 1032
 <212> PRT
 <213> Canis familiaris

<400> 21

```

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
1           5           10           15

```

```

Ala Ala Ala Leu Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
          20           25           30

```

```

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
          35           40           45

```

```

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Pro Arg Gly Asn
50           55           60

```

```

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
65           70           75           80

```

Tyr Asp Phe Val His Phe Val His Leu Arg Arg Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
 100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Asp Leu
 115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
 130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
 145 150 155 160

Ala Thr Leu Ala Gly Leu Tyr Ala Leu Arg Phe Leu Phe Leu Asp Gly
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Leu Gln Val Ala Pro
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Val Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Gly Phe
 260 265 270

Pro Gln Leu His Pro Asn Thr Phe Gly His Leu Ser His Leu Glu Gly
 275 280 285

Leu Val Leu Arg Asp Ser Ser Leu Tyr Ser Leu Asp Pro Arg Trp Phe
 290 295 300

His Gly Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro

545	550	555	560
Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu	565	570	575
Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg	580	585	590
Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser	595	600	605
Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg	610	615	620
Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn	625	630	635
Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser	645	650	655
Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp	660	665	670
Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly	675	680	685
Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln	690	695	700
Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro	705	710	715
Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala	725	730	735
Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly	740	745	750
Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys	755	760	765
Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro	770	775	780

Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly
 785 790 795 800

Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu
 805 810 815

Ser Trp Val Cys Phe Ser Leu Ser Leu Leu Ala Val Ala Leu Ser Leu
 820 825 830

Ala Val Pro Met Leu His Gln Leu Cys Gly Trp Asp Leu Trp Tyr Cys
 835 840 845

Phe His Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Arg Gly
 850 855 860

Val Asp Ala Leu Ala Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln
 865 870 875 880

Ser Ser Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Gln Leu Glu
 885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp
 900 905 910

Trp Val Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr
 915 920 925

Ser Ser Arg Lys Thr Leu Phe Val Leu Ala Arg Thr Asp Arg Val Ser
 930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Cys Pro Asp Ala His
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
 980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln
 995 1000 1005

Leu Gly Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Thr Ala
 1025 1030

<210> 22
 <211> 822
 <212> PRT
 <213> Canis familiaris

<400> 22

Met Gly Pro Cys Arg Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Ala Leu Ala Leu Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
 20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Pro Arg Gly Asn
 50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
 65 70 75 80

Tyr Asp Phe Val His Phe Val His Leu Arg Arg Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
 100 105 110

Thr Ile Glu Pro Asn Thr Phe Leu Ala Val Pro Thr Leu Glu Asp Leu
 115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
 130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
 145 150 155 160

Ala Thr Leu Ala Gly Leu Tyr Ala Leu Arg Phe Leu Phe Leu Asp Gly
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Gln Gln Ala Leu Gln Val Ala Pro
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Val Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Arg Glu Cys Pro Lys Gly Phe
 260 265 270

Pro Gln Leu His Pro Asn Thr Phe Gly His Leu Ser His Leu Glu Gly
 275 280 285

Leu Val Leu Arg Asp Ser Ser Leu Tyr Ser Leu Asp Pro Arg Trp Phe
 290 295 300

His Gly Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Lys Ala Phe Tyr Gly Leu Ala Arg Leu
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
 340 345 350

His Leu His Leu Ala Ser Ser Phe Gly Ser Leu Leu Ser Leu Gln Glu
 355 360 365

Leu Asp Ile His Gly Ile Phe Phe Arg Ser Leu Ser Lys Thr Thr Leu
 370 375 380

Gln Ser Leu Ala His Leu Pro Met Leu Gln Arg Leu His Leu Gln Leu
 385 390 395 400

Asn Phe Ile Ser Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ala Glu
 420 425 430

Pro Ala Ala Ala Thr Gly Glu Val Glu Ala Asp Cys Gly Glu Arg Val
 435 440 445

Trp Pro Gln Ser Arg Asp Leu Ala Leu Gly Pro Leu Gly Thr Pro Gly
 450 455 460

Ser Glu Ala Phe Met Pro Ser Cys Arg Thr Leu Asn Phe Thr Leu Asp
 465 470 475 480

Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Val Arg
 485 490 495

Leu Ala Arg Leu Gln Cys Leu Gly Leu Ser His Asn Ser Ile Ser Gln
 500 505 510

Ala Val Asn Gly Ser Gln Phe Val Pro Leu Ser Asn Leu Arg Val Leu
 515 520 525

Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr
 530 535 540

Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro
 545 550 555 560

Phe Ser Met Arg Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu
 565 570 575

Pro Ala Leu Arg Tyr Leu Ser Leu Ala His Asn Gly Ile His Ser Arg
 580 585 590

Val Ser Gln Gln Leu Arg Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser
 595 600 605

Gly Asn Thr Leu Ser Gln Met Trp Ala Glu Gly Asp Leu Tyr Leu Arg
 610 615 620

Phe Phe Gln Gly Leu Arg Ser Leu Val Gln Leu Asp Leu Ser Gln Asn
 625 630 635 640

Arg Leu His Thr Leu Leu Pro Arg Asn Leu Asp Asn Leu Pro Lys Ser
 645 650 655

Leu Arg Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp

660

665

670

Ser Ser Leu Ala Leu Leu Pro Lys Leu Glu Ala Leu Asp Leu Ala Gly
 675 680 685

Asn Gln Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln
 690 695 700

Leu Gln Arg Leu Asp Leu Ser Gly Asn Ser Ile Gly Phe Val Val Pro
 705 710 715 720

Ser Phe Phe Ala Leu Ala Val Arg Leu Arg Glu Leu Asn Leu Ser Ala
 725 730 735

Asn Ala Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly
 740 745 750

Ala Leu Lys Val Leu Asp Val Thr Ala Asn Pro Leu His Cys Ala Cys
 755 760 765

Gly Ala Thr Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro
 770 775 780

Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly
 785 790 795 800

Arg Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu
 805 810 815

Ser Trp Val Cys Phe Ser
 820

<210> 23

<211> 3334

<212> DNA

<213> Canis familiaris

<400> 23

aggaaggggc tgtgagctcc aagcatcctt tcctgcagct gctgcccagc ctgccagcca 60
 gaccctctgg agaagcccc gctccctgtc atggggccct gccgtggcgc cctgcacccc 120
 ctgtctctcc tggtgcaggc tgccgcgcta gccctggccc tggcccaggg caccctgcct 180
 gccttcctgc cctgtgagct ccagcccat ggcctggtga actgcaactg gctgttcctc 240
 aagtccgtgc cccgcttctc ggcagctgca ccccgcggtg acgtcaccag cctttccttg 300

tactccaacc gcatccacca cctccatgac tatgactttg tccacttcgt ccacctgcgg	360
cgtctcaatc tcaagtggaa ctgcccgcgc gccagcctca gcccacatgca ctttccctgt	420
cacatgacca ttgagcccaa caccttcctg gctgtgcccc ccctagagga cctgaatctg	480
agctataaca gcatcacgac tgtgcccgcg ctgcccagtt cgcttgtgtc cctgtccctg	540
agccgcacca acatcctggg gctggaccct gccaccctgg caggccttta tgccttgccg	600
ttcctgttcc tggatggcaa ctgctactac aagaaccctt gccagcaggc cctgcagggtg	660
gcccaggtg cctcctggg cctgggcaac ctccacacacc tgtcactcaa gtacaacaac	720
ctcaccgtgg tgccgcgggg cctgcccccc agcctggagt acctgctctt gtcctacaac	780
cacatcatca ccctggcacc tgaggacctg gccaatctga ctgccctgcg tgcctcgat	840
gtgggtggga actgtcgccg ctgtgacct gcccgtaacc cctgcaggga gtgcccacag	900
ggcttcccc agctgcaccc caacaccttc ggccacctga gccacctcga aggcctgggtg	960
ttgagggaca gctctctcta cagcctggac ccaggtgggt tccatggcct gggcaacctc	1020
atggtgctgg acctgagtga gaacttcctg tatgactgca tcaccaaacc caaagccttc	1080
tacggcctgg ccggtgctgc cagactcaac ctgtccttca attatcataa gaagggtgtc	1140
tttgeccacc tgcactctggc atcctccttc gggagcctac tgcctctgca ggagctggac	1200
atacatggca tcttcttccg ctgctcagc aagaccacgc tccagtcgct ggcccacctg	1260
cccatgctcc agcgtctgca tctgcagttg aactttatca gccaggccca gctcagcatc	1320
ttcgggcct tccctggact gcggtacgtg gacttgtcag acaaccgcat cagtggagct	1380
gcagagcccc cggtgcccac aggggaggta gaggcagact gtggggagag agtctggcca	1440
cagtccccggg accttgcctt gggcccactg ggcacccccg gctcagaggc cttcatgccg	1500
agctgcagga ccctcaactt caccttggac ctgtctcgga acaacctagt gactgttcag	1560
ccggagatgt ttgtccggct ggcgcgcctc cagtgcctgg gcctgagcca caacagcatc	1620
tcgcaggcgg tcaatggctc gcagttcgtg cctctgagca acctgcgggt gctggacctg	1680
tcccataaca agctggacct gtaccacggg cgctcgttca cggagctgcc gcggctggag	1740
gccttggacc tcagctacaa cagccagccc ttcagcatgc ggggcgtggg ccacaatctc	1800
agctttgtgg cacagctgcc agccctgcgc tacctcagcc tggcgcacaa tggcatccac	1860
agccgcgtgt cccagcagct ccgcagcgcc tcgctccggg ccctggactt cagtggcaat	1920
accctgagcc agatgtgggc cgaggagac ctctatctcc gcttcttcca aggcctgaga	1980
agcctgggtc agctggacct gtcccagaat cgcttcgata ccctcctgcc acgcaacctg	2040
gacaacctcc ccaagagcct ggcgtcctg cggtccgtg acaattacct ggctttcttc	2100

aactggagca gcctggccct cctacccaag ctggaagccc tggacctggc gggaaaccag 2160
ctgaaggccc tgagcaatgg cagcttgccc aacggcacc cagctccagag gctggacctc 2220
agcggcaaca gcatcggctt cgtgggtcccc agcttttttg ccttggccgt gaggcttcga 2280
gagctcaacc tcagcgccaa cgccctcaag acgggtggagc cctcctgggtt tggttccctg 2340
gcggttgccc tgaaagtcct agacgtgacc gccaaacctt tgcattgcgc ttgcggcgca 2400
accttcgtgg acttcttgct ggaggtgcag gctgcgggtgc cgggcctgcc tagccgtgtc 2460
aagtgcggca gcccgggcca gctccagggc cgcagcatct tcgcacagga cctgcgcctc 2520
tgcctggacg aagcgtcttc ctgggtctgt ttcagcctct cgtctgtggc tgtggccctg 2580
agcctggctg tgcccatgct gcaccagctc tgtggctggg acctctggta ctgcttcac 2640
ctgtgcctgg cctggctgcc cggcgggggg cggcgggggg gtgtggatgc cctggcctat 2700
gacgccttcg tggcttcga caaggcgcag agctcgggtg cggactgggt gtacaatgag 2760
ctgcgggtac agctagagga ggcgcgtggg cgcgggggc tacgcctgtg tctggaggaa 2820
cgtgactggg taccggcaa aacctcttc gagaacctct gggcctcagt ttacagcagc 2880
cgcaagacgc tgtttgctgct ggccgcacg gacagagtc gggcctcct gcgtgccagc 2940
ttcctgctgg cccaacagcg cctgctggag gaccgcaagg acgtcgtggg gctgggtgatc 3000
ctgtgccccg acgcccaccg ctcccgctat gtgcggctgc gccagcgctt ctgcccag 3060
agtgtcctcc tctggcccca ccagcccagt ggccagcgca gcttctgggc ccagctgggc 3120
acggcctga ccagggacaa ccgccacttc tacaaccaga acttctgccg gggccccacg 3180
acagcctgat aggcagacag ccagcacct tcgcgcccct acacctgcc tgtctgtctg 3240
ggatgccga cctgctgggt ctacaccgcc gctctgtctc ccctacacc agccctggca 3300
taaagcgacc gctcaataaa tgctgctggg agac 3334

<210> 24

<211> 2466

<212> DNA

<213> *Canis familiaris*

<400> 24

atgggcccct gccgtggcg cctgcacccc ctgtctctcc tgggtgcaggc tgccgcgcta 60
gccctggccc tggcccaggg caccctgctt gccttcctgc cctgtgagct ccagcccat 120
ggcctgggtga actgcaactg gctgttcttc aagtccgtgc cccgcttctc ggcagctgca 180
ccccgcggta acgtcaccag cctttccttg tactccaacc gcatccacca cctccatgac 240
tatgactttg tccacttcgt ccacctgcgg cgtctcaatc tcaagtggaa ctgcccgcc 300

gccagcctca gccccatgca ctttccctgt cacatgacca ttgagcccaa caccttcctg	360
gctgtgcca ccctagagga cctgaatctg agctataaca gcatcacgac tgtgcccgcc	420
ctgcccagtt cgcttgtgtc cctgtccctg agccgcacca acatcctggg gctggaccct	480
gccaccctgg caggccttta tgccctgcgc ttctgttcc tggatggcaa ctgctactac	540
aagaaccct gccagcaggc cctgcagggt gccccagggt ccctcctggg cctgggcaac	600
ctcacacacc tgtcactcaa gtacaacaac ctaccgtgg tgccgcgggg cctgcccccc	660
agcctggagt acctgctctt gtcctacaac cacatcatca ccctggcacc tgaggacctg	720
gccaatctga ctgccctgcg tgcctcgat gtgggtggga actgtcgccg ctgtgaccat	780
gcccgttaacc cctgcaggga gtgcccgaag ggcttcccc agctgcaccc caacaccttc	840
ggccacctga gccacctcga aggcctgggt ttgaggga gctctctcta cagcctggac	900
cccagggtgg tccatggcct gggcaacctc atgggtgctg acctgagtga gaacttcctg	960
tatgactgca tcacaaaac caaagccttc tacggcctgg ccgggtgcg cagactcaac	1020
ctgtccttca attatcataa gaagggtgcc tttgccacc tgcactggc atcctccttc	1080
gggagcctac tgtccctgca ggagctggac atacatggca tcttcttccg ctgctcagc	1140
aagaccacgc tccagtcgt ggccacctg cccatgctcc agcgtctgca tctgcagttg	1200
aactttatca gccaggcca gctcagcatc ttcgggcct tccctggact gcggtacgtg	1260
gacttgtcag acaaccgcat cagtggagct gcagagccc cggtgccac aggggaggta	1320
gaggcagact gtggggagag agtctggcca cagtcccggg accttgctct gggcccactg	1380
ggcaccoccg gctcagaggc cttcatgccg agctgcagga ccctcaactt caccttggac	1440
ctgtctcgga acaacctagt gactgttcag ccggagatgt ttgtccggct ggcgcgctc	1500
cagtgcctgg gcctgagcca caacagcatc tcgcaggcgg tcaatggctc gcagttcgtg	1560
cctctgagca acctgcgggt gctggacctg tcccataaca agctggacct gtaccacggg	1620
cgctcgttca cggagctgcc gcggctggag gccttgacc tcagctaaa cagccagccc	1680
ttcagcatgc ggggcgtggg ccacaatctc agctttgtgg cacagctgcc agccctgcgc	1740
tacctagcc tggcgcaaaa tggcatccac agccgcgtgt cccagcagct ccgcagcgcc	1800
tcgctccggg ccctggactt cagtggcaat accctgagcc agatgtgggc cgaggagac	1860
ctctatctcc gcttcttcca aggcctgaga agcctgggtc agctggacct gtcccagaat	1920
cgctgcata ccctcctgcc acgcaacctg gacaacctcc ccaagagcct gcggctcctg	1980
cggctccgtg acaattacct ggctttcttc aactggagca gcctggccct cctaccaag	2040

```

ctggaagccc tggacctggc gggaaaccag ctgaaggccc tgagcaatgg cagcttgccc 2100
aacggcaccc agctccagag gctggacctc agcggcaaca gcatcggctt cgtggtcccc 2160
agcttttttg ccctggccgt gaggttcga gagctcaacc tcagcgccaa cgccctcaag 2220
acggtggagc cctcctggtt tggttccctg gcggtgccc tgaaagtctt agacgtgacc 2280
gccaaaccct tgcattgcgc ttgcggcgca accttcgtgg acttcttgct ggaggtgcag 2340
gctgcggtgc ccggcctgcc tagccgtgtc aagtgcggca gcccgggcca gctccagggc 2400
cgcagcatct tcgcacagga cctgcgcctc tgcttgagc aagcgtcttc ctgggtctgt 2460
ttcagc 2466

```

<210> 25

<211> 1031

<212> PRT

<213> Felis catus

<400> 25

```

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
1          5          10          15

```

```

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
20          25          30

```

```

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu
35          40          45

```

```

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn
50          55          60

```

```

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
65          70          75          80

```

```

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp
85          90          95

```

```

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
100          105          110

```

```

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
115          120          125

```

```

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
130          135          140

```

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
 145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe
 260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe
 290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Gln Leu
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
 340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu
 370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met
385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu
420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu
435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu
450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser
465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser
485 490 495

Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val
500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala
565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser
580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe

610	615	620
Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu		
625	630	635 640
His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg		
	645	650 655
Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser		
	660	665 670
Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln		
	675	680 685
Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln		
	690	695 700
Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe		
705	710	715 720
Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala		
	725	730 735
Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu		
	740	745 750
Lys Val Leu Asp Val Thr Gly Asn Pro Leu His Cys Ala Cys Gly Ala		
	755	760 765
Ala Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu		
	770	775 780
Pro Gly His Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser		
785	790	795 800
Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp		
	805	810 815
Asp Cys Phe Gly Leu Ser Leu Leu Thr Val Ala Leu Gly Leu Ala Val		
	820	825 830
Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His		
	835	840 845

Leu Cys Leu Ala Trp Leu Pro Arg Arg Gly Arg Arg Arg Gly Ala Asp
 850 855 860

Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala
 865 870 875 880

Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg
 885 890 895

Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu
 900 905 910

Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr Ser Ser
 915 920 925

Arg Lys Met Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu
 930 935 940

Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg
 945 950 955 960

Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His Arg Ser
 965 970 975

Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Leu
 980 985 990

Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly
 995 1000 1005

Thr Ala Leu Thr Arg Asp Asn Gln His Phe Tyr Asn Gln Asn Phe
 1010 1015 1020

Cys Arg Gly Pro Thr Thr Ala Glu
 1025 1030

<210> 26
 <211> 820
 <212> PRT
 <213> Felis catus

<400> 26

Met Gly Pro Cys His Gly Ala Leu His Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Ala Leu Ala Val Ala Leu Ala Gln Gly Thr Leu Pro Ala Phe
 20 25 30

Leu Pro Cys Glu Leu Gln Arg His Gly Leu Val Asn Cys Asp Trp Leu
 35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Ala Ala Ala Pro Arg Gly Asn
 50 55 60

Val Thr Ser Leu Ser Leu Tyr Ser Asn Arg Ile His His Leu His Asp
 65 70 75 80

Ser Asp Phe Val His Leu Ser Ser Leu Arg Arg Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Ala Ser Leu Ser Pro Met His Phe Pro Cys His Met
 100 105 110

Thr Ile Glu Pro His Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
 115 120 125

Asn Leu Ser Tyr Asn Ser Ile Thr Thr Val Pro Ala Leu Pro Ser Ser
 130 135 140

Leu Val Ser Leu Ser Leu Ser Arg Thr Asn Ile Leu Val Leu Asp Pro
 145 150 155 160

Ala Asn Leu Ala Gly Leu His Ser Leu Arg Phe Leu Phe Leu Asp Gly
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Pro Gln Ala Leu Gln Val Ala Pro
 180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Ala Val Pro Arg Gly Leu Pro Pro Ser Leu Glu Tyr
 210 215 220

Leu Leu Leu Ser Tyr Asn His Ile Ile Thr Leu Ala Pro Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Arg Asn Pro Cys Met Glu Cys Pro Lys Gly Phe
 260 265 270

Pro His Leu His Pro Asp Thr Phe Ser His Leu Asn His Leu Glu Gly
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Tyr Asn Leu Asn Pro Arg Trp Phe
 290 295 300

His Ala Leu Gly Asn Leu Met Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Tyr Asp Cys Ile Thr Lys Thr Thr Ala Phe Gln Gly Leu Ala Gln Leu
 325 330 335

Arg Arg Leu Asn Leu Ser Phe Asn Tyr His Lys Lys Val Ser Phe Ala
 340 345 350

His Leu His Leu Ala Pro Ser Phe Gly Ser Leu Leu Ser Leu Gln Gln
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Ser Glu Thr Thr Leu
 370 375 380

Arg Ser Leu Val His Leu Pro Met Leu Gln Ser Leu His Leu Gln Met
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Ala Phe Pro Gly
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Met Glu
 420 425 430

Leu Ala Ala Ala Thr Gly Glu Val Asp Gly Gly Glu Arg Val Arg Leu
 435 440 445

Pro Ser Gly Asp Leu Ala Leu Gly Pro Pro Gly Thr Pro Ser Ser Glu
 450 455 460

Gly Phe Met Pro Gly Cys Lys Thr Leu Asn Phe Thr Leu Asp Leu Ser
 465 470 475 480

Arg Asn Asn Leu Val Thr Ile Gln Pro Glu Met Phe Ala Arg Leu Ser
 485 490 495

Arg Leu Gln Cys Leu Leu Leu Ser Arg Asn Ser Ile Ser Gln Ala Val
 500 505 510

Asn Gly Ser Gln Phe Met Pro Leu Thr Ser Leu Gln Val Leu Asp Leu
 515 520 525

Ser His Asn Lys Leu Asp Leu Tyr His Gly Arg Ser Phe Thr Glu Leu
 530 535 540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser
 545 550 555 560

Met Gln Gly Val Gly His Asn Leu Ser Phe Val Ala Gln Leu Pro Ala
 565 570 575

Leu Arg Tyr Leu Ser Leu Ala His Asn Asp Ile His Ser Arg Val Ser
 580 585 590

Gln Gln Leu Cys Ser Ala Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
 595 600 605

Ala Leu Ser Arg Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe
 610 615 620

Arg Gly Leu Arg Ser Leu Val Arg Leu Asp Leu Ser Gln Asn Arg Leu
 625 630 635 640

His Thr Leu Leu Pro Arg Thr Leu Asp Asn Leu Pro Lys Ser Leu Arg
 645 650 655

Leu Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Asn Trp Ser Ser
 660 665 670

Leu Val Leu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ala Gly Asn Gln
 675 680 685

Leu Lys Ala Leu Ser Asn Gly Ser Leu Pro Asn Gly Thr Gln Leu Gln
 690 695 700

Arg Leu Asp Leu Ser Ser Asn Ser Ile Ser Phe Val Ala Ser Ser Phe
 705 710 715 720

Phe Ala Leu Ala Thr Arg Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala

725

730

735

Leu Lys Thr Val Glu Pro Ser Trp Phe Gly Ser Leu Ala Gly Thr Leu
 740 745 750

Lys Val Leu Asp Val Thr Gly Asn Pro Leu His Cys Ala Cys Gly Ala
 755 760 765

Ala Phe Val Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
 770 775 780

Pro Gly His Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
 805 810 815

Asp Cys Phe Gly
 820

<210> 27
 <211> 3235
 <212> DNA
 <213> Felis catus

<400> 27
 aggggtctgcg agctccaggc attcttctct gccatcgctg cccagtctgc catccagacc 60
 ctctggagaa gccccactc cctgtcatgg gccctgcca tggcgccctg cccccctgt 120
 ctctcctggg gcaggetgcc gcgctggccg tggccctggc ccagggcacc ctgcctgcct 180
 ttctgcccctg tgagctccag cgccacggcc tgggtgaattg cgactggctg ttcctcaagt 240
 ccgtgccccca cttctcggcg gcagcgcccc gtggtaacgt caccagcctt tccctgtact 300
 ccaaccgcat ccaccacctc cactgactccg actttgtcca cctgtccagc ctgcggcgctc 360
 tcaacctcaa atggaactgc ccaccgcca gcctcagccc catgcacttc ccctgtcaca 420
 tgaccattga gcccacacc ttccctggccg tgcccaccct ggaggagctg aacctgagct 480
 acaacagcat cagcagagta cccgcccctgc ccagttccct cgtgtcccctg tccttgagcc 540
 gtaccaacat cctgggtgctg gaccctgcca acctgcagg gctgcactcc ctgcgctttc 600
 tgttcctgga tggcaactgc tactacaaga acccctgccc gcaggccctg caggtggccc 660
 cgggcgccct ccttggcctg ggcaacctta cgcacctgtc actcaagtac aacaacctca 720
 ctgcggtgcc ccgcggcctg cccccagcc tggagtacct gctattgtcc tacaaccaca 780

tcataccacct	ggcacctgag	gacctggcca	acctgaccgc	cctgcgtgtg	ctcgatgtgg	840
gtgggaactg	ccgtcgctgt	gaccacgccc	gcaaccctg	tatggagtgc	cccaagggct	900
tcccgacact	gcaccctgac	accttcagcc	acctgaacca	cctcgaaggc	ctggtgttga	960
aggacagctc	tctctacaac	ctgaacccca	gatggttcca	tgccctgggc	aacctcatgg	1020
tgctggacct	gagtgagaac	ttcctatatg	actgcatcac	caaaaccaca	gccttccagg	1080
gcctggccca	gctgcgcaga	ctcaacttgt	ctttcaatta	ccacaagaag	gtgtcctttg	1140
cccacctgca	tctggcgccc	tccttcggga	gcctgctctc	cctgcagcag	ctggacatgc	1200
atggcatctt	cttcgcctcg	ctcagcgaga	ccacgctccg	gtcgctggtc	cacctgcccc	1260
tgctccagag	tctgcacctg	cagatgaact	tcatcaatca	ggcccagctc	agcatcttcg	1320
gggccttccc	tggcctgcca	tacgtggacc	tgctcagaaa	ccgcataagt	ggagccatgg	1380
agctggcggc	tgccacgggg	gaggtggatg	gtggggagag	agtccggctg	ccatctgggg	1440
acctagctct	gggcccaccg	ggcaccctta	gctccgaggg	cttcatgcca	ggctgcaaga	1500
ccctcaactt	caccttgga	ctgtcacgga	acaacctagt	gacaatccag	ccagagatgt	1560
ttgcccggct	ctcgcgctc	cagtgcctgc	tcctgagccg	caacagcatc	tcgcaggcag	1620
tcaacggctc	acaatttatg	ccgctgacca	gcctgcaggt	gctggacctg	tcccataaca	1680
agctggacct	gtaccatggg	cgctctttca	cggagctgcc	gcggctggag	gccctggacc	1740
tcagctacaa	cagccagccc	ttcagcatgc	agggcgtggg	tcacaacctc	agctttgtgg	1800
cacagctgcc	ggccctgcgc	tatctcagcc	tggcgcacaa	cgacatccac	agccgtgtgt	1860
cccagcagct	ctgcagcgcc	tcgctgcggg	ccttggactt	cagcggcaat	gccttgagcc	1920
ggatgtgggc	cgagggagac	ctgtatctcc	acttcttccg	aggcctgagg	agcctgggtcc	1980
ggttggatct	gtcccagaat	cgctgcata	ccctcttgcc	acgcaccctg	gacaacctcc	2040
ccaagagcct	gcggctgctg	cgctctccgtg	acaattatct	ggctttcttc	aactggagca	2100
gcctggtcct	cctccccagg	ctggaagccc	tggacctggc	gggaaaccag	ctgaaggccc	2160
tgagcaacgg	cagcttgcc	aatggaaccc	agctccagag	gctggacctc	agcagcaaca	2220
gtatcagctt	cgtggcctcc	agcttttttg	ctctggccac	caggctgcga	gagctcaacc	2280
tcagtgccaa	cgcctcaag	acggtggagc	cctcctgggt	cggttctcta	gcgggcaccc	2340
tgaaagtcct	agatgtgact	ggcaaccccc	tgactgcgc	ctgtggggcg	gccttcgtgg	2400
acttcttgct	ggaggtgcag	gctgcagtgc	ccggcctgcc	aggccacgtc	aagtgtggca	2460
gtccaggtca	gctccagggc	cgcagcatct	ttgcgcagga	tctgcgcctc	tgccctggatg	2520
agggcctctc	ctgggactgt	tttggcctct	cgctgctgac	cgtggccctg	ggcctggccg	2580

tgcccatgct gcaccacctc tgtggctggg acctctggta ctgcttccac ctgtgcctgg 2640
 cctggctgcc ccggcggggg cggcggcggg gcgcggatgc cctgccctac gatgcctttg 2700
 tggctcttga caaggcacag agcgcggtgg ccgactgggt gtacaacgag ctgcgggtac 2760
 ggctagagga gcgccgtgga cgccgagcgc tccgcctgtg cctggaggaa cgtgactggc 2820
 tacccggtaa aacgctcttt gagaacctgt gggcctcagt ttacagcagc cgcaagatgc 2880
 tgtttgtgct ggccacaca gacaggggtca gcggcctctt gcgcgccagc tttctgctgg 2940
 ccagcagcg cctgctggag gaccgcaagg acgttgtggt gctgggtgatc ctgcgccccg 3000
 acgcccaccg ctcccgtat gtgcggctgc gccagcgcct ctgccgccag agcgtcctcc 3060
 tctggcccca ccagcccagt ggccagcgca gcttctgggc ccagctgggc acggccctga 3120
 ccagggacaa ccagcacttc tataaccaga acttctgccg gggccccacg acggcagagt 3180
 gaccgcccag caccccaagc ctctacacc ttgcctgtct gcctgggatg ccggg 3235

<210> 28
 <211> 2460
 <212> DNA
 <213> *Felis catus*

<400> 28
 atgggcccct gccatggcgc cctgcacccc ctgtctctcc tgggtgcaggc tgccgcgctg 60
 gccgtggccc tggcccaggg caccctgcct gcctttctgc cctgtgagct ccagcgccac 120
 ggcttgggtga attgcgactg gctgttcttc aagtccgtgc ccacttctc ggcggcagcg 180
 ccccgtygta acgtcaccag cctttccctg tactccaacc gcatccacca cctccacgac 240
 tccgactttg tccacctgtc cagcctgcgg cgtctcaacc tcaaattggaa ctgcccaccc 300
 gccagcctca gcccctatgca cttcccctgt cacatgacca ttgagcccca caccttctctg 360
 gccgtgcca ccctggagga gctgaacctg agctacaaca gcatcacgac agtaccgcgc 420
 ctgcccagtt cctcgtgtc cctgtccttg agccgtacca acatcctggg gctggaccct 480
 gccaacctcg cagggtgca ctccctgcgc tttctgttcc tggatggcaa ctgctactac 540
 aagaaccct gccgcaggc cctgcagggt gcccggggcg cctccttg cctgggcaac 600
 cttacgcacc tgtcactcaa gtacaacaac ctactgcgg tgccccgcgg cctgcccccc 660
 agcctggagt acctgctatt gtccataaac cacatcatca ccctggcacc tgaggacctg 720
 gccaacctga ccgcctgcg tgtgctcgat gtgggtggga actgccgtcg ctgtgaccac 780
 gcccgaacc cctgtatgga gtgcccgaag ggcttccgc acctgcacc tgacaccttc 840
 agccacctga accacctga aggcctggtg ttgaaggaca gctctctcta caacctgaac 900


```

cccagatggg tccatgccct gggcaacctc atgggtgctgg acctgagtga gaacttccta      960
tatgactgca tcacaaaaac cacagccttc cagggcctgg cccagctgcg cagactcaac    1020
ttgtctttca attaccacaa gaaggtgtcc ttgcccacc tgcattctggc gccctccttc    1080
gggagcctgc tctccctgca gcagctggac atgcatggca tcttcttccg ctgcgtcagc    1140
gagaccacgc tccggctcgt ggtccacctg cccatgctcc agagtctgca cctgcagatg    1200
aacttcatca atcaggccca gctcagcatc ttccggggcct tccctggcct gcgatacgtg    1260
gacctgtcag acaaccgcat aagtggagcc atggagctgg cggctgccac gggggaggtg    1320
gatggtgggg agagagtccg gctgccatct ggggacctag ctctgggccc accgggcacc    1380
cctagctccg agggcttcat gccaggctgc aagacctca acttcacctt ggacctgtca    1440
cggaacaacc tagtgacaat ccagccagag atgtttgccc ggctctcgcg cctccagtgc    1500
ctgctcctga gccgcaacag catctcgagc gcagtcaacg gctcacaatt tatgccgctg    1560
accagcctgc aggtgctgga cctgtcccat aacaagctgg acctgtacca tgggcgctct    1620
ttcacggagc tgccgaggct ggaggccctg gacctcagct acaacagcca gcccttcagc    1680
atgcagggcg tgggtcacia cctcagcttt gtggcacagc tgccggccct gcgctatctc    1740
agcctggcgc acaacgacat ccacagccgt gtgtcccagc agctctgcag cgcctcgtg    1800
cgggccttgg acttcagcgg caatgccttg agccggatgt gggccgaggg agacctgtat    1860
ctccacttct tccgaggcct gaggagcctg gtccgggttg atctgtccca gaatcgctg    1920
cataccctct tgccacgcac cctggacaac ctccccaaaga gcctgcggct gctgcgtctc    1980
cgtgacaatt atctggcttt cttcaactgg agcagcctgg tctctctccc caggctggaa    2040
gccctggacc tggcgggaaa ccagctgaag gccctgagca acggcagctt gcctaatagga    2100
accagctcc agaggctgga cctcagcagc aacagtatca gcttcgtggc ctccagcttt    2160
tttgctctgg ccaccaggct gcgagagctc aacctcagtg ccaacgccct caagacggtg    2220
gagccctcct ggttcgggtc tctagcgggc accctgaaag tcttagatgt gactggcaac    2280
cccctgcact gcgcctgtgg ggcggccttc gtggacttct tgctggaggt gcaggctgca    2340
gtgcccggcc tgccaggcca cgtcaagtgt ggcagtccag gtcagctcca gggccgcagc    2400
atctttgcgc aggatctgcg cctctgcctg gatgaggccc tctcctggga ctgttttggc    2460

```

```

<210> 29
<211> 1032
<212> PRT
<213> Mus musculus

```

<400> 29

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn
 50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn
 65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met
 100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
 130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
 145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro
 180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
 210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu

225		230		235		240
Ala Asn Leu Thr Ser	Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg					
	245		250		255	
Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser						
	260		265		270	
Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly						
	275		280		285	
Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe						
	290		295		300	
Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu						
305		310		315		320
Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu						
	325		330		335	
Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala						
	340		345		350	
Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu						
	355		360		365	
Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu						
	370		375		380	
Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met						
385		390		395		400
Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala						
	405		410		415	
Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr						
	420		425		430	
Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu						
	435		440		445	
Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser						
	450		455		460	

Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu
 465 470 475 480

Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
 485 490 495

Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala
 500 505 510

Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp
 515 520 525

Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu
 530 535 540

Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
 545 550 555 560

Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser
 565 570 575

Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val
 580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly
 595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe
 610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn
 625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu
 645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr
 660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn
 675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
 690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala
 705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn
 725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
 740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly
 755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly
 770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg
 785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser
 805 810 815

Trp Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Met Val
 820 825 830

Val Pro Ile Leu His His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe
 835 840 845

His Leu Cys Leu Ala Trp Leu Pro Leu Leu Ala Arg Ser Arg Arg Ser
 850 855 860

Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln
 865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu
 885 890 895

Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp
 900 905 910

Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr
 915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser
 930 935 940

Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
 980 985 990

Leu Phe Trp Pro Gln Gln Pro Asn Gly Gln Gly Gly Phe Trp Ala Gln
 995 1000 1005

Leu Ser Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln
 1010 1015 1020

Asn Phe Cys Arg Gly Pro Thr Ala Glu
 1025 1030

<210> 30
 <211> 821
 <212> PRT
 <213> Mus musculus

<400> 30

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
 1 5 10 15

Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
 20 25 30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
 35 40 45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn
 50 55 60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn
 65 70 75 80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp
 85 90 95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met
 100 105 110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu
 115 120 125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
 130 135 140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
 145 150 155 160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly
 165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro
 180 185 190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
 210 215 220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser
 260 265 270

Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe
 290 295 300

Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu
 325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala

340	345	350
Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu		
355	360	365
Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu		
370	375	380
Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met		
385	390	395 400
Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala		
	405	410 415
Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr		
	420	425 430
Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu		
	435	440 445
Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser		
	450	455 460
Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu		
465	470	475 480
Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu		
	485	490 495
Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala		
	500	505 510
Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp		
	515	520 525
Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu		
	530	535 540
Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe		
545	550	555 560
Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser		
	565	570 575

Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val
580 585 590

Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly
595 600 605

Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe
610 615 620

Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn
625 630 635 640

Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu
645 650 655

Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr
660 665 670

Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn
675 680 685

Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
690 695 700

Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala
705 710 715 720

Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn
725 730 735

Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
740 745 750

Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly
755 760 765

Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly
770 775 780

Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg
785 790 795 800

Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser
805 810 815

Trp Asp Cys Phe Gly
820

<210> 31

<211> 3200

<212> DNA

<213> Mus musculus

<400> 31

tgtcagaggg agcctcggga gaatcctcca tctcccaaca tggttctccg tcgaaggact	60
ctgcacccct tgtccctcct ggtacaggct gcagtgctgg ctgagactct ggccctgggt	120
accctgcctg ccttcctacc ctgtgagctg aagcctcatg gcctgggtgga ctgcaattgg	180
ctgttcctga agtctgtacc ccgtttctct gcggcagcat cctgctccaa catcaccgcg	240
ctctccttga tctccaaccg tatccaccac ctgcacaact ccgacttcgt ccacctgtcc	300
aacctgcggc agctgaacct caagtggaac tgtccacca ctggccttag cccctgcac	360
ttctcttgcc acatgaccat tgagcccaga accttctctg ctatgcgtac actggaggag	420
ctgaacctga gctataatgg tatcaccact gtgccccgac tgcccagctc cctggtgaat	480
ctgagcctga gccacaccaa catcctgggt ctagatgcta acagcctcgc cggcctatac	540
agcctgcgcg ttctcttcat ggacgggaac tgctactaca agaaccctg cacaggagcg	600
gtgaagggtga cccagggcg cctcctgggc ctgagcaatc tcacccatct gtctctgaag	660
tataacaacc tcacaaagggt gccccgcaa ctgccccca gcctggagta cctcctgggtg	720
tcctataacc tcattgtcaa gctggggcct gaagacctg ccaatctgac ctcccttoga	780
gtacttgatg tgggtgggaa ttgccgtcgc tgcgacctg cccccaatcc ctgtatagaa	840
tgtggccaaa agtccctcca cctgcacct gagaccttcc atcacctgag ccatctggaa	900
ggcctgggtgc tgaaggacag ctctctccat aactgaact cttcctgggt ccaaggctctg	960
gtcaacctct cgggtgctgga cctaagcgag aactttctct atgaaagcat caaccacacc	1020
aatgcctttc agaacctaac ccgcctgcgc aagctcaacc tgtccttcaa ttaccgcaag	1080
aaggatatcct ttgcccgcct ccacctggca agttccttca agaacctgggt gtcactgcag	1140
gagctgaaca tgaacggcat cttcttccgc tcgctcaaca agtacacgct cagatggctg	1200
gccgatctgc ccaaactcca cactctgcat cttcaaata acttcatcaa ccaggcacag	1260
ctcagcatct ttggtacctt ccgagccctt cgctttgtgg acttgtcaga caatcgcac	1320
agtgggcctt caacgctgtc agaagccacc cctgaagagg cagatgatgc agagcaggag	1380
gagctgttgt ctgcggatcc tcaccagct ccactgagca cccctgcttc taagaacttc	1440

atggacaggt gtaagaactt caagttcacc atggacctgt ctcggaacaa cctggtgact	1500
atcaagccag agatgtttgt caatctctca cgctccagt gtcttagcct gagccacaac	1560
tccattgcac aggctgtcaa tggctctcag ttcttgccgc tgactaatct gcagggtgctg	1620
gacctgtccc ataacaaact ggacttgtag cactggaaat cgttcagtga gctaccacag	1680
ttgcaggccc tggacctgag ctacaacagc cagcccttta gcatgaaggg tataggccac	1740
aatttcagtt ttgtggccca tctgtccatg ctacacagcc ttagcctggc acacaatgac	1800
attcataccc gtgtgtcctc acatctcaac agcaactcag tgaggtttct tgacttcagc	1860
ggcaacggta tgggccgcat gtgggatgag gggggccttt atctccattt cttccaaggc	1920
ctgagtggcc tgctgaagct ggacctgtct caaaataacc tgcatatcct ccggccccag	1980
aaccttgaca acctcccaa gagcctgaag ctgctgagcc tccgagacaa ctacctatct	2040
ttctttaact ggaccagtct gtccttcctg cccaacctgg aagtcctaga cctggcaggc	2100
aaccagctaa aggccctgac caatggcacc ctgcctaata gacacctcct ccagaaactg	2160
gatgtcagca gcaacagtat cgtctctgtg gtcccagcct tcttcgctct ggcggtcgag	2220
ctgaaagagg tcaacctcag ccacaacatt ctcaagacgg tggatcgctc ctggtttggg	2280
cccatgtgta tgaacctgac agttctagac gtgagaagca accctctgca ctgtgcctgt	2340
ggggcagcct tcgtagactt actgttggag gtgcagacca aggtgcctgg cctggctaata	2400
ggtgtgaagt gtggcagccc cggccagctg cagggccgta gcatcttcgc acaggacctg	2460
cggctgtgcc tggatgaggt cctctcttgg gactgctttg gcctttcact cttggctgtg	2520
gccgtgggca tgggtggtgcc tatactgcac catctctgcg gctgggacgt ctggtactgt	2580
tttcatctgt gcctggcatg gctacctttg ctggcccgca gccgacgcag cggccaagct	2640
ctccctatg atgccttcgt ggtgttcgat aaggcacaga gcgcagttgc ggactgggtg	2700
tataacgagc tgcgggtgcg gctggaggag cggcgcggtc gccgagccct acgcttgtgt	2760
ctggaggacc gagattggct gcctggccag acgctcttcg agaacctctg ggcttccatc	2820
tatgggagcc gcaagactct atttgtgctg gccacacgg accgcgtcag tggcctcctg	2880
cgcaccagct tctgtctggc tcagcagcgc ctgttggaaag accgcaagga cgtggtggtg	2940
ttggtgatcc tgcgtccgga tgcccaccgc tcccgtatg tgcgactgcg ccagcgtctc	3000
tgccgccaga gtgtgctctt ctggccccag cagcccaacg ggcagggggg cttctgggcc	3060
cagctgagta cagccctgac tagggacaac cgccaattct ataaccagaa cttctgccgg	3120
ggacctacag cagaatagct cagagcaaca gctggaaaca gctgcatctt catgcctggt	3180
tcccagttg ctctgctgc	3200

<210> 32
 <211> 2463
 <212> DNA
 <213> Mus musculus

<400> 32
 atggtttctcc gtcgaaggac tctgcacccc ttgtccctcc tggtagagga tgcagtgtg 60
 gctgagactc tggccctggg taccctgcct gccttcctac cctgtgagct gaagcctcat 120
 ggcctgggtg actgcaattg gctgttcctg aagtctgtac cccgtttctc tgcggcagca 180
 tctgtctcca acatcacccg cctctccttg atctccaacc gtatccacca cctgcacaac 240
 tccgacttcg tccacctgtc caacctgcgg cagctgaacc tcaagtggaa ctgtccaccc 300
 actggcctta gccccctgca cttctcttgc cacatgacca ttgagcccag aacottcctg 360
 gctatgcgta cactggagga gctgaacctg agctataatg gtatcaccac tgtgccccga 420
 ctgcccagct ccctggtgaa tctgagcctg agccacacca acatcctggg tctagatgct 480
 aacagcctcg ccggcctata cagcctgcgc gttctcttca tggacgggaa ctgctactac 540
 aagaaccctt gcacaggagc ggtgaagggtg accccaggcg ccctcctggg cctgagcaat 600
 ctcacccatc tgtctctgaa gtataacaac ctcacaaagg tgccccgcca actgcccccc 660
 agcctggagt acctcctggg gtcctataac ctcattgtca agctggggcc tgaagacctg 720
 gccaatctga cctcccttcg agtacttgat gtgggtggga attgccgtcg ctgcgaccat 780
 gcccccaatc cctgtataga atgtggccaa aagtcctcc acctgcaccc tgagaccttc 840
 catcacctga gccatctgga aggcctgggtg ctgaaggaca gctctctcca tacactgaac 900
 tcttctctgg tccaaggtct ggtcaacctc tcgggtgctg acctaagcga gaactttctc 960
 tatgaaagca tcaaccacac caatgccttt cagaacctaa ccgcctgcg caagctcaac 1020
 ctgtccttca attaccgcaa gaaggtatcc tttgcccgcc tccacctggc aagttccttc 1080
 aagaacctgg tgtcactgca ggagctgaac atgaacggca tcttcttccg ctgcgtcaac 1140
 aagtagacgc tcagatggct ggccgatctg cccaaactcc acactctgca tcttcaaagt 1200
 aacttcatca accaggcaca gctcagcatc tttggtacct tccgagccct tcgctttgtg 1260
 gacttgctag acaatcgcat cagtgggcct tcaacgctgt cagaagccac ccctgaagag 1320
 gcagatgatg cagagcagga ggagctgttg tctgcggatc ctcaccagc tccactgagc 1380
 acccctgctt ctaagaactt catggacagg tgtaagaact tcaagttcac catggacctg 1440
 tctcggaaca acctgggtgac tatcaagcca gagatgtttg tcaatctctc acgcctccag 1500
 tgtcttagcc tgagccacaa ctccattgca caggctgtca atggctctca gttcctgcg 1560

```

ctgactaatc tgcaggtgct ggacctgtcc cataacaaac tggacttgta ccactggaaa 1620
tcgttcagtg agctaccaca gttgcaggcc ctggacctga gctacaacag ccagcccttt 1680
agcatgaagg gtataggcca caatttcagt tttgtggccc atctgtccat gctacacagc 1740
cttagcctgg cacacaatga cattcatacc cgtgtgtcct cacatctcaa cagcaactca 1800
gtgaggtttc ttgacttcag cggcaacggt atgggccgca tgtgggatga ggggggcctt 1860
tatctccatt tcttccaagg cctgagtggc ctgctgaagc tggacctgtc tcaaaataac 1920
ctgcatatcc tccggcccca gaaccttgac aacctccca agagcctgaa gctgctgagc 1980
ctccgagaca actacctatc tttctttaac tggaccagtc tgtccttcct gcccaacctg 2040
gaagtccctag acctggcagg caaccagcta aaggccctga ccaatggcac cctgcctaata 2100
ggcacccctcc tccagaaact ggatgtcagc agcaacagta tcgtctctgt ggtcccagcc 2160
ttcttcgctc tggcggtcga gctgaaagag gtcaacctca gccacaacat tctcaagacg 2220
gtggatcgct cctggtttgg gccattgtg atgaacctga cagttctaga cgtgagaagc 2280
aaccctctgc actgtgcctg tggggcagcc ttcgtagact tactgttgga ggtgcagacc 2340
aagggtgcctg gcctggctaa tgggtgtgaag tgtggcagcc ccggccagct gcagggccgt 2400
agcatcttcg cacaggacct gcggctgtgc ctggatgagg tcctctcttg ggactgcttt 2460
ggc 2463

```

```

<210> 33
<211> 1032
<212> PRT
<213> Homo sapiens
<400> 33

```

```

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln
1           5           10           15

```

```

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20           25           30

```

```

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
35           40           45

```

```

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn
50           55           60

```

```

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp
65           70           75           80

```

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu

305		310		315		320
Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu						
		325		330		335
Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala						
		340		345		350
His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu						
		355		360		365
Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu						
		370		375		380
Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met						
		385		390		400
Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly						
		405		410		415
Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu						
		420		425		430
Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu						
		435		440		445
Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu						
		450		455		460
Asp Phe Arg Pro Asn Cys Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser						
		465		470		475
Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser						
		485		490		495
His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val						
		500		505		510
Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu						
		515		520		525
Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu						
		530		535		540

Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly
 545 550 555 560

Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr
 565 570 575

Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser
 580 585 590

Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn
 595 600 605

Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe
 610 615 620

Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu
 625 630 635 640

His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln
 645 650 655

Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser
 660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg
 675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg
 690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe
 705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
 725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu
 740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
 755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
 805 810 815

Asp Cys Phe Ala Leu Ser Leu Leu Ala Val Ala Leu Gly Leu Gly Val
 820 825 830

Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His
 835 840 845

Leu Cys Leu Ala Trp Leu Pro Trp Arg Gly Arg Gln Ser Gly Arg Asp
 850 855 860

Glu Asp Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Thr Gln
 865 870 875 880

Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Gly Gln Leu Glu
 885 890 895

Glu Cys Arg Gly Arg Trp Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp
 900 905 910

Trp Leu Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr
 915 920 925

Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser
 930 935 940

Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
 945 950 955 960

Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Gly Arg
 965 970 975

Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
 980 985 990

Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln
 995 1000 1005

Leu Gly Met Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg
 1010 1015 1020

Asn Phe Cys Gln Gly Pro Thr Ala Glu
1025 1030

<210> 34
<211> 820
<212> PRT
<213> Homo sapiens

<400> 34

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln
1 5 10 15

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20 25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
35 40 45

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn
50 55 60

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp
65 70 75 80

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp
85 90 95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met
100 105 110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
115 120 125

Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser
130 135 140

Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser
145 150 155 160

Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly
165 170 175

Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro
180 185 190

Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205

Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr
 210 215 220

Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu
 225 230 235 240

Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255

Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe
 260 265 270

Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
 275 280 285

Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe
 290 295 300

Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320

Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu
 325 330 335

Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala
 340 345 350

His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu
 355 360 365

Leu Asp Met His Gly Ile Phe Phe Arg Ser Leu Asp Glu Thr Thr Leu
 370 375 380

Arg Pro Leu Ala Arg Leu Pro Met Leu Gln Thr Leu Arg Leu Gln Met
 385 390 395 400

Asn Phe Ile Asn Gln Ala Gln Leu Gly Ile Phe Arg Ala Phe Pro Gly
 405 410 415

Leu Arg Tyr Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Ala Ser Glu

420	425	430
Leu Thr Ala Thr Met Gly Glu Ala Asp Gly Gly Glu Lys Val Trp Leu		
435	440	445
Gln Pro Gly Asp Leu Ala Pro Ala Pro Val Asp Thr Pro Ser Ser Glu		
450	455	460
Asp Phe Arg Pro Asn Cys Ser Thr Leu Asn Phe Thr Leu Asp Leu Ser		
465	470	475
		480
Arg Asn Asn Leu Val Thr Val Gln Pro Glu Met Phe Ala Gln Leu Ser		
485	490	495
His Leu Gln Cys Leu Arg Leu Ser His Asn Cys Ile Ser Gln Ala Val		
500	505	510
Asn Gly Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu		
515	520	525
Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu		
530	535	540
Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Gly		
545	550	555
		560
Met Gln Gly Val Gly His Asn Phe Ser Phe Val Ala His Leu Arg Thr		
565	570	575
Leu Arg His Leu Ser Leu Ala His Asn Asn Ile His Ser Gln Val Ser		
580	585	590
Gln Gln Leu Cys Ser Thr Ser Leu Arg Ala Leu Asp Phe Ser Gly Asn		
595	600	605
Ala Leu Gly His Met Trp Ala Glu Gly Asp Leu Tyr Leu His Phe Phe		
610	615	620
Gln Gly Leu Ser Gly Leu Ile Trp Leu Asp Leu Ser Gln Asn Arg Leu		
625	630	635
		640
His Thr Leu Leu Pro Gln Thr Leu Arg Asn Leu Pro Lys Ser Leu Gln		
645	650	655

Val Leu Arg Leu Arg Asp Asn Tyr Leu Ala Phe Phe Lys Trp Trp Ser
 660 665 670

Leu His Phe Leu Pro Lys Leu Glu Val Leu Asp Leu Ala Gly Asn Arg
 675 680 685

Leu Lys Ala Leu Thr Asn Gly Ser Leu Pro Ala Gly Thr Arg Leu Arg
 690 695 700

Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe
 705 710 715 720

Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala
 725 730 735

Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu
 740 745 750

Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala
 755 760 765

Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu
 770 775 780

Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser
 785 790 795 800

Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp
 805 810 815

Asp Cys Phe Ala
 820

<210> 35

<211> 3352

<212> DNA

<213> Homo sapiens

<400> 35

aggctggtat aaaaatctta cttcctctat tctctgagcc gctgctgccc ctgtgggaag 60

ggacctcgag tgtgaagcat ccttcctgt agctgctgtc cagtctgccc gccagaccct 120

ctggagaagc ccctgcccc cagcatgggt ttctgccgca gcgccctgca cccgctgtct 180

ctcctgggtgc aggccatcat gctggccatg accctggccc tgggtacctt gcctgccttc 240

ctaccctgtg agctccagcc ccacggcctg gtgaactgca actggctgtt cctgaagtct 300

gtgccccact tctccatggc agcaccccgt ggcaatgtca ccagcctttc cttgtcctcc	360
aaccgcatcc accacctcca tgattctgac tttgcccacc tgcccagcct gcggcatctc	420
aacctcaagt ggaactgccc gccggttggc ctcagcccca tgcaattccc ctgccacatg	480
accatcgagc ccagcacctt cttggctgtg cccaccctgg aagagctaaa cctgagctac	540
aacaacatca tgactgtgcc tgcgctgccc aaatccctca tatccctgtc cctcagccat	600
accaacatcc tgatgctaga ctctgccagc ctcgccggcc tgcatgccct gcgcttccta	660
ttcatggacg gcaactgtta ttacaagaac ccctgcaggc aggcactgga ggtggccccg	720
ggtgccctcc ttggcctggg caacctcacc cacctgtcac tcaagtacaa caacctcact	780
gtggtgcccc gcaacctgcc ttccagcctg gagtatctgc tgttgtccta caaccgcatc	840
gtcaaactgg cgcctgagga cctggccaat ctgaccgccc tgcgtgtgct cgatgtgggc	900
ggaaattgcc gccgctgcga ccacgctccc aacctctgca tggagtgcct tcgtcacttc	960
ccccagctac atcccgatac cttcagccac ctgagccgtc ttgaaggcct ggtgttgaag	1020
gacagttctc tctcctggct gaatgccagt tggttccgtg ggctgggaaa cctccgagt	1080
ctggacctga gtgagaactt cctctacaaa tgcactacta aaaccaaggc cttccagggc	1140
ctaacacagc tgcgcaaget taacctgtcc ttcaattacc aaaagagggt gtcctttgcc	1200
cacctgtctc tggccccctc cttcgggagc ctggctgccc tgaaggagct ggacatgcac	1260
ggcatcttct tccgctcact cgatgagacc acgctccggc cactggcccg cctgcccattg	1320
ctccagactc tgcgtctgca gatgaacttc atcaaccagg cccagctcgg catcttcagg	1380
gccttccttg gcctgcgcta cgtggacctg tcggacaacc gcatcagcgg agcttcggag	1440
ctgacagcca ccatggggga ggcagatgga ggggagaagg tctggctgca gcctggggac	1500
cttgctccgg cccagtgga cactcccagc tctgaagact tcaggcccaa ctgcagcacc	1560
ctcaacttca ccttgatct gtcacggaac aacctggtga ccgtgcagcc ggagatgttt	1620
gccagctct cgcacctgca gtgcctgcgc ctgagccaca actgcatctc gcaggcagtc	1680
aatggctccc agttcctgcc gctgaccggt ctgcagggtc tagacctgtc ccgcaataag	1740
ctggacctct accacgagca ctcatcacg gagctaccgc gactggaggc cctggacctc	1800
agctacaaca gccagccctt tggcatgcag ggcgtgggccc acaacttcag cttcgtggct	1860
cacctgcgca ccctgcgcca cctcagcctg gccacaaca acatccacag ccaagtgtcc	1920
cagcagctct gcagtacgtc gctgcgggccc ctggacttca gcggcaatgc actgggcat	1980
atgtgggccc agggagacct ctatctgcac ttcttccaag gcctgagcgg tttgatctgg	2040

ctggacttgt cccagaaccg cctgcacacc ctctgcccc aaaccctgcg caacctcccc 2100
 aagagcctac aggtgctgcg tctccgtgac aattacctgg ccttctttaa gtggtggagc 2160
 ctccacttcc tgcccaaact ggaagtccct gacctggcag gaaaccggct gaaggccctg 2220
 accaatggca gcctgcctgc tggcaccggt ctccggaggc tggatgtcag ctgcaacagc 2280
 atcagcttcg tggcccccg cttcttttcc aaggccaagg agctgcgaga gctcaacctt 2340
 agcgccaacg ccctcaagac agtggaccac tcctggtttg ggcccctggc gagtgccttg 2400
 caaatactag atgtaagcgc caaccctctg cactgcgctt gtggggcggc ctttatggac 2460
 ttctgtctgg aggtgcaggc tgccgtgccc ggtctgcca gccgggtgaa gtgtggcagt 2520
 ccggggccagc tccagggcct cagcatcttt gcacaggacc tgcgctcttg cctggatgag 2580
 gccctctcct gggactgttt cgccctctcg ctgctggctg tggctctggg cctgggtgtg 2640
 cccatgctgc atcacctctg tggctgggac ctctggtact gcttcacct gtgcctggcc 2700
 tggcttccct ggcgggggcg gcaaagtggg cgagatgagg atgccctgcc ctacgatgcc 2760
 ttcgtggtct tcgacaaaac gcagagcgca gtggcagact ggggtgtacaa cgagcttcgg 2820
 gggcagctgg aggagtgccg tgggcgctgg gcactccgcc tgtgcctgga ggaacgcgac 2880
 tggctgcctg gcaaaaccct ctttgagaac ctgtgggcct cggctctatgg cagccgcaag 2940
 acgctgtttg tgctggccca cacggaccgg gtcagtggtc tcttgcgcg cagcttccctg 3000
 ctggcccagc agcgctgct ggaggaccgc aaggacgtcg tggtgctggt gatcctgagc 3060
 cctgacggcc gccgctcccg ctacgtgcgg ctgcgccagc gcctctgccg ccagagtgtc 3120
 ctctcttgcc cccaccagcc cagtggctag cgcagcttct gggcccagct gggcatggcc 3180
 ctgaccaggg acaaccacca cttctataac cggaacttct gccagggacc cacggccgaa 3240
 tagccgtgag ccggaatcct gcacgggtgcc acctccacac tcacctcacc tctgcctgcc 3300
 tggctctgacc ctcccctgct cgcctccctc accccacacc tgacacagag ca 3352

<210> 36

<211> 2460

<212> DNA

<213> Homo sapiens

<400> 36

atgggtttct gccgcagcgc cctgcaccgc ctgtctctcc tgggtgcaggc catcatgctg 60
 gccatgacct tggccctggg taccttgctt gccttcctac cctgtgagct ccagccccac 120
 ggctggtga actgcaactg gctgttcctg aagtctgtgc ccaacttctc catggcagca 180
 ccccggtggca atgtcaccag cttttccttg tcctccaacc gcatccacca cctccatgat 240

tctgactttg cccacctgcc cagcctgcgg catctcaacc tcaagtggaa ctgcccgcg	300
gttggcctca gcccacatgca cttcccctgc cacatgacca tcgagcccag caccttcttg	360
gctgtgcca ccctggaaga gctaaacctg agctacaaca acatcatgac tgtgcctgcg	420
ctgccc aaat ccctcatatc cctgtccctc agccatacca acatcctgat gctagactct	480
gccagcctcg ccggcctgca tgccctgcgc ttccatttca tggacggcaa ctgttattac	540
aagaaccct gcaggcaggc actggagggtg gccccgggtg ccctccttgg cctgggcaac	600
ctcaccacc tgtcactcaa gtacaacaac ctactgtgg tgccccgcaa cctgccttcc	660
agcctggagt atctgctgtt gtccataaac cgcacgtca aactggcgcc tgaggacctg	720
gccaatctga ccgccctgcg tgtgctcgat gtggcgaggaa attgccgcg ctgcgaccac	780
gtccccaacc cctgcatgga gtgccctcgt cacttcccc agctacatcc cgataccttc	840
agccacctga gccgtcttga aggcctggtg ttgaaggaca gttctctctc ctggctgaat	900
gccagttggt tccgtgggtt gggaaacctc cgagtgtgtg acctgagtga gaacttctc	960
tacaaatgca tcaactaaaac caaggccttc cagggcctaa cacagctgcg caagcttaac	1020
ctgtccttca attacaaaa gaggggtgtc tttgccacc tgtctctggc cccttcttc	1080
gggagcctgg tcgccctgaa ggagctggac atgcacggca tcttcttccg ctactcgat	1140
gagaccacgc tccggccact ggcccgctg cccatgtcc agactctgcg tctgcagatg	1200
aacttcatca accaggccca gctcggcatc ttcaggcct tcctggcct gcgtacgtg	1260
gacctgtcgg acaaccgcat cagcggagct tcggagctga cagccaccat gggggaggca	1320
gatggagggg agaaggtctg gctgcagcct ggggacctt ctccggcccc agtggacact	1380
cccagctctg aagacttcag gcccaactgc agcacctca acttcacctt ggatctgtca	1440
cggaaacaacc tggtgaccgt gcagccggag atgtttgcc agctctcgca cctgcagtgc	1500
ctgcgcctga gccacaactg catctcgag gcagtcaatg gctcccagtt cctgccgctg	1560
accggtctgc aggtgctaga cctgtccgc aataagctgg acctctacca cgagcactca	1620
ttcacggagc taccgcgact ggaggcctg gacctcagct acaacagcca gccctttggc	1680
atgcagggcg tgggccacaa cttcagcttc gtggctcacc tgcgaccct gcgccacctc	1740
agcctggccc acaacaacat ccacagccaa gtgtcccagc agctctgcag tacgtcgctg	1800
cgggccctgg acttcagcgg caatgcactg ggccatatgt gggccgaggg agacctctat	1860
ctgcacttct tccaaggcct gagcggtttg atctggctgg acttgcccc gaaccgcctg	1920
cacaccctcc tgcccaaac cctgcgcaac ctccccaga gcctacaggt gctgcgtctc	1980
ctgacaatt acctggcctt ctttaagtgg tggagcctcc acttctgcc caaactggaa	2040

gtcctcgacc tggcaggaaa ccggctgaag gccctgacca atggcagcct gcctgctggc 2100
 acccggtccc ggaggctgga tgtcagctgc aacagcatca gcttcgtggc ccccggttc 2160
 ttttccaagg ccaaggagct gcgagagctc aaccttagcg ccaacgccct caagacagtg 2220
 gaccactcct ggtttgggccc cctggcgagt gccctgcaaa tactagatgt aagcgccaac 2280
 cctctgcact gcgcctgtgg ggcgcccttt atggacttcc tgctggaggt gcaggctgcc 2340
 gtgcccggtc tgcccagccg ggtgaagtgt ggcatccgg gccagctcca gggcctcagc 2400
 atctttgcac aggacctgcg cctctgcctg gatgaggccc tctcctggga ctgtttcgcc 2460

<210> 37
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 37
 accttgccctg ccttcctacc ctgtga 26

<210> 38
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 38
 gtccgtgtgg gccagcacia a 21

<210> 39
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 39
 tccatgacgt ttttgatgtt 20

<210> 40
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 40
tccataacgt ttttgatggt 20

<210> 41
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 41
tccatcacgt ttttgatggt 20

<210> 42
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 42
tccattacgt ttttgatggt 20

<210> 43
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 43
tccatggcgt ttttgatggt 20

<210> 44
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 44
tccatgccgt ttttgatggt 20

<210> 45
<211> 20
<212> DNA
<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 45

tccatgtcgt ttttgatggt

20

<210> 46

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 46

tccatgatgt ttttgatggt

20

<210> 47

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 47

tccatgaagt ttttgatggt

20

<210> 48

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 48

tccatgaggt ttttgatggt

20

<210> 49

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 49

tccatgacat ttttgatggt

20

<210> 50

<211> 20

<212> DNA

<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 50
tccatgacct ttttgatggt 20

<210> 51
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 51
tccatgactt ttttgatggt 20

<210> 52
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 52
tccatgacgc ttttgatggt 20

<210> 53
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 53
tccatgacga ttttgatggt 20

<210> 54
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 54
tccatgacgg ttttgatggt 20

<210> 55
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 55
tccatgacgt ctttgatggt 20

<210> 56
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 56
tccatgacgt atttgatggt 20

<210> 57
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 57
tccatgacgt gtttgatggt 20

<210> 58
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 58
tcgtcgtttt gtcgttttgt cggt 24

<210> 59
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 59
tgctgctttt gtgcttttgt gctt 24

<210> 60
<211> 20
<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 60

tccatgacgt tcctgatgct

20

<210> 61

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 61

tccatgagct tcctgatgct

20

<210> 62

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> Consensus oligopeptide

<220>

<221> MISC_FEATURE

<222> (4)..(5)

<223> Any amino acid

<220>

<221> MISC_FEATURE

<222> (7)..(12)

<223> Any amino acid

<220>

<221> MISC_FEATURE

<222> (14)..(15)

<223> Any amino acid

<400> 62

Gly Asn Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys
1 5 10 15

<210> 63

<211> 16

<212> PRT

<213> Homo sapiens

<400> 63

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys
 1 5 10 15

<210> 64
 <211> 16
 <212> PRT
 <213> Mus musculus

<400> 64

Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys Met Ile Cys
 1 5 10 15

<210> 65
 <211> 31
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Consensus oligopeptide

<220>
 <221> MISC_FEATURE
 <222> (2)..(8)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (10)..(10)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (12)..(12)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (14)..(22)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (25)..(30)
 <223> Any amino acid

<400> 65

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Asp Xaa Tyr Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Ser Xaa Xaa Xaa Xaa Xaa Tyr
 20 25 30

<210> 66
 <211> 31
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (2)..(8)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (10)..(10)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (12)..(12)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (14)..(22)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (25)..(30)
 <223> Any amino acid

<400> 66

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Xaa Xaa Xaa Xaa Xaa Tyr
 20 25 30

<210> 67
 <211> 31
 <212> PRT
 <213> Mus musculus

<220>
 <221> MISC_FEATURE
 <222> (2)..(8)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (10)..(10)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (12)..(12)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (14)..(22)
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> (25)..(30)
 <223> Any amino acid

<400> 67

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Asp Xaa Tyr Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Gln Leu Xaa Xaa Xaa Xaa Xaa Xaa Tyr
 20 25 30

<210> 68
 <211> 31
 <212> PRT
 <213> Homo sapiens

<400> 68

Gln Val Leu Asp Leu Ser Arg Asn Lys Leu Asp Leu Tyr His Glu His
 1 5 10 15

Ser Phe Thr Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser Tyr
 20 25 30

<210> 69
 <211> 31
 <212> PRT
 <213> Mus musculus

<400> 69

Gln Val Leu Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys

1 5 10 15

Ser Phe Ser Glu Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr
 20 25 30

```
<210> 70
<211> 20
<212> DNA
<213> Artificial sequence
```

<220>
<223> Synthetic oligonucleotide

```
<400> 70
tccaggactt ctctcaggtt 20
```